

CCACGGCTCCCGTCAGCTCTCGTTCCGAGAAAGCAGCGCGCTCGCCCTCGGGCCATCCCGGGGAATGGGC
CCCCCTCGTACCTAGTGTTCGCGGGGCAAAAAGGGTCTTCGCGCGCTCGCTCGTGCAGGGGCTAT
CTGGGCGCCCTGAGCGCGCGCTCGGAGCCCTTGGAGCCCGCCGAGCGGGGGCACACCCGGGAACCT
GCTGAGCGCGCGGGACCATGACCGGGGAGGCCATCTGCAGCGCGCCCTCGCCACCATTCCTCTACCA
GAACTCCCGACCTCGCTACCTGAGCCCGGGCGCTTGGCACTGTGTCTCGCGCGCGCGCGCCACG
GAGACTGGCGCGTCCAGGTGGCGCTGAAGCAGCTGACATCCACACTCCGCTCGCTGACAGTGA
AGAAAGCATGTCTTAAGAGAAGCTGAAATTTTACACAAAGCTAGATTTAGTTACATTCCTTCAT
TTTGGGAATTTCAATGAGCGCTGAAATTTTGGGAATAGTTACTGAAATACATGCGCAATGATCAT
TAAATGAACCTCTACATAGGAAAACTCAATATCTCTGATGTTGCTTGGCCATTGAGATTTCTTATC
CTGCATGAAATTCGCGCTTGGTGTAAATTAAGCTGACAAATATGACTCCTCTTACTTCTCATCTGA
CTTGAAGACTCAGAATATCTTATTCGACAAATTTCTATGTTTGAAGTTGAGATTTTGGTTTAT
CAAAGTGGCGCATGATGTCTCTCAGCTCAGCAAGTAGCAATCTGCACGAAAGGAGGGGACA
ATTATCTATATGCCACCTCAAAACTATGAACCTGGACAAAAATCAAGGGCCAGTATCAAGCACGA
TATATATAGCTATGCAGTTATCAGATGGGAAGTGTATCCAGAAAACAGCCTTTTGAAGATGTCA
CCAATCCTTTGCAGATAATGTATAGTGTGTCAAGGACATCCACCTGTTATTTAATGAAGAAAGT
TTGCCATATGATATACCTCAGCGAGCAGTATGATCTCTTAATAGAAAGTGGATGGGCACAAAA
TCCAGATGAAAGACCATCTTTCTTAAATGTTTATAGAACTTCAACCAAGTTTTSAGAACATTTG
AAGAGATAACTTTCTTGAAGCTTCTTATTCAGCTAAAGAAAAACAAAGTTACAGAGTGTTCAGT
GCCATTCACTATGTGACAGAGAGAAAAATGGAATTTCTCTCAACATACCTGTAATCATGGTCC
ACAAGAGGAATCATGTGATCTCTCAGCTGCAATGAAAAATAGTGGTTCTCTGAAACTTCAAGGT
GCTGCGCAGCTCTTCAAGACAAATGATTTTCTTATGAAAGCTCAAGACTTTTATTTTATGAAG
CTGCATCACTGTCTTGGAAATCAGCTTGGGATAGCACCTTTCTGGATCTCAAAGGGGCTGCATT
CTGTGATCACAAGACCATTTCTATGCTCTTCAAGCAATTAATAATCCACTCTCAACTGAGGAACT
CAGAACGTCTGAGCCTGGTATAGCCGAGGAGTGGATCCGAGCAAAAGGGAAGACATTTGTGAAC
CAAATGACAGAAGCCTGCTTACCAGTCTGCTAGATGCCCTTCTGTCCAGGGGACTTATCATGAA
AGAGGACTATGAACTTGTAGTACCAAGCCCTCAAGGACCTCAAAAGTCAGACAATTACTAGACA
CTACTGACATCCAAGGAGAAGAAATTTGCCAAAGTTATAGTACAAAAATTGAAAGATACAAACAA
ATGGGTCTTCAGCCTTACCCGGAATACTTGTGGTTCTAGATCACCATCTTAAATTTACTTCA
AAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGAAATGTGTTTCAATAAAGGATATTTATAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:1)

FIG. 1

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Met	Asn	Gly	Glu	Ala	Ile	Cys	Ser	Ala	Leu	Pro	Thr	Ile	Pro	Tyr	His	Lys	Leu	Ala	Asp	10
Leu	Arg	Tyr	Leu	Ser	Arg	Gly	Ala	Ser	Gly	Thr	Val	Ser	Ser	Ala	Arg	His	Ala	Asp	Tyr	40
Arg	Val	Gln	Val	Ala	Val	Lys	His	Leu	His	Ile	His	Thr	Pro	Leu	Leu	Asp	Ser	Gln	Arg	60
Lys	Asp	Val	Leu	Arg	Glu	Ala	Glu	Ile	Leu	His	Lys	Ala	Arg	Phe	Ser	Tyr	Ile	Leu	Pro	80
Ile	Leu	Gly	Ile	Cys	Asn	Glu	Pro	Glu	Phe	Leu	Gly	Ile	Val	Thr	Glu	Tyr	Met	Pro	Asn	100
Gly	Ser	Leu	Asn	Glu	Leu	Leu	His	Arg	Lys	Thr	Glu	Tyr	Pro	Asp	Val	Ala	Tyr	Pro	Leu	120
Arg	Phe	Arg	Ile	Leu	His	Glu	Ile	Ala	Leu	Gly	Val	Asn	Tyr	Leu	His	Asn	Met	Thr	Pro	140
Pro	Leu	Leu	His	His	Asp	Leu	Lys	Thr	Gln	Asn	Ile	Leu	Leu	Asp	Asn	Glu	Phe	His	Val	160
Lys	Ile	Ala	Asp	Phe	Gly	Leu	Ser	Lys	Tyr	Arg	Met	Met	Ser	Leu	Ser	Gln	Ser	Arg	Ser	180
Ser	Lys	Ser	Ala	Pro	Glu	Gly	Gly	Thr	Ile	Ile	Tyr	Met	Pro	Pro	Glu	Asn	Tyr	Gln	Pro	200
Gly	Gln	Lys	Ser	Arg	Ala	Ser	Ile	Lys	His	Asp	Ile	Tyr	Ser	Tyr	Ala	Val	Ile	Thr	Tyr	220
Ile	Val	Leu	Ser	Arg	Lys	Gln	Pro	Phe	Glu	Asp	Val	Thr	Asn	Pro	Leu	Gln	Ile	Met	Tyr	240
Ser	Val	Ser	Gln	Gly	His	Arg	Pro	Val	Ile	Asn	Glu	Glu	Ser	Leu	Pro	Tyr	Asp	Ile	Pro	260
His	Arg	Ala	Arg	Met	Ile	Ser	Leu	Ile	Glu	Ser	Gly	Tyr	Ala	Gln	Asn	Pro	Asp	Glu	Arg	280
Pro	Ser	Phe	Leu	Lys	Cys	Leu	Ile	Glu	Leu	Glu	Pro	Val	Leu	Arg	Thr	Phe	Glu	Gln	Ile	300
Thr	Phe	Leu	Glu	Ala	Val	Ile	Gln	Leu	Lys	Lys	Thr	Lys	Leu	Gln	Ser	Val	Ser	Ser	Ala	320
Ile	His	Leu	Cys	Asp	Lys	Lys	Lys	Met	Glu	Leu	Ser	Leu	Asn	Ile	Pro	Val	Asn	His	Gly	340
Pro	Gln	Glu	Glu	Ser	Cys	Gly	Ser	Ser	Gln	Leu	His	Glu	Asn	Ser	Gly	Ser	Pro	Glu	Thr	360
Ser	Arg	Ser	Leu	Pro	Ala	Pro	Gln	Asp	Asn	Asp	Phe	Leu	Ser	Arg	Lys	Ala	Gln	Asp	Cys	380
Tyr	Phe	Met	Lys	Leu	His	His	Cys	Pro	Gly	Asn	His	Ser	Tyr	Asp	Ser	Thr	Ile	Ser	Gly	400
Ser	Gln	Arg	Ala	Ala	Phe	Cys	Asp	His	Lys	Thr	Ile	Pro	Cys	Ser	Ser	Ala	Ile	Ile	Asn	420
Pro	Leu	Ser	Thr	Ala	Gly	Asn	Ser	Glu	Arg	Leu	Gln	Pro	Gly	Ile	Ala	Gln	Gln	Tyr	Ile	440
Gln	Ser	Lys	Arg	Glu	Asp	Ile	Val	Asn	Gln	Met	Thr	Glu	Ala	Cys	Leu	Asn	Gln	Ser	Leu	460
Asp	Ala	Leu	Leu	Ser	Arg	Asp	Leu	Ile	Met	Lys	Glu	Asp	Tyr	Glu	Leu	Val	Ser	Thr	Lys	480
Pro	Thr	Arg	Thr	Ser	Lys	Val	Arg	Gln	Leu	Leu	Asp	Thr	Thr	Asp	Ile	Gln	Gly	Glu	Glu	500
Phe	Ala	Lys	Val	Ile	Val	Gln	Lys	Leu	Lys	Asp	Asn	Lys	Gln	Met	Gly	Leu	Gln	Pro	Tyr	520
Pro	Glu	Ile	Leu	Val	Val	Ser	Arg	Ser	Pro	Ser	Leu	Asn	Leu	Leu	Gln	Asn	Lys	Ser	Met	540

(SEQ ID NO:2)

FIG. 2

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TTTTATGGG AATGCCAGCT TGGAGAGAC AGARCAATTC GAGAAWAAA TTTAAATTC
 AGATTACCC AATGTTGTTT TAAAATATTC TAACTTCAAA GAATGATGCC AGAAGCTTAA
 AAGGGRCTTC GCAGAGTAGC AGGGGGGCTT GAGGGGGGGG CCTGAATCCT GATTGGGCTT
 TTCTGAGAG GACACAGGCA GCTGAAGATG AATTGGGAA AAGTAGCCGC TTCTACTTT
 AACTATGGA GAGCAGGGCC AGAGTGAGAT GGAATATTC CCATCAGAGT CTCACCCCA
 CATTCAATTA CTGAAAAGCA ATCGGGAATC TCTGTCAGT CACATCCGCA ATACTCAGTG
 TCTGCTGAC AACTTCTCTA AGAATGACTA CTTCTCGGCC GAAGATGCCG AGATTCTGTG
 TCCCTCGCCC ACCCAGCCTG ACAAGGTCCG CAAAATTCTG GACCTGCTAC AGAGCAAGGG
 CGAGGAGGTG TCCGAGTTCT TCTCTACTTT GCTCCAGCAA CTGCGAGATG CCTACGTGCA
 CCTCAGGCTT TGGTCTCTGG AGATCGGCTT CTGCGCTTCC CTGCTCACTC AGAGCAAAGT
 CTGCTCAAC ACTGACCCAG TTAGCAGGTA TACCGAGCAG CTGCGACACC ATCTGGGCC
 TCACTCAAG TTCTGCTCTT CTTATGCCCA GAAGGAGGAG CTGCTGCTGG AGGAGATCTA
 CATGGACACC ATCATGGAGC TGGTTGGCTT CAGCAATGAG AGCCTGGGCA GCCTGAACAG
 CTTGGCCTGC CTCTGGAGC ACACCAAGCG CATCTCTAAT GAGCAGGGTG AGACCATCTT
 CATCTCTGGT GATGCTGGGG TGGCAAGTC CATGCTGCTA CAGCGGCTGC AGAGCCTCTG
 GGCCACGGGC CGGCTAGAGC CAGGGGTCAA ATTCTTCTTC CACTTTGCTT GCGGCATGTT
 CAGCTCTTC AAGGAAAGTG ACAGGCTGTG TCTGCAGGAC CTGCTCTTCA AGCACTACTG
 CTACCCAGAG CGGGACCCCG AGGAGGTGTT TGGCTTCTG CTGCGCTTCC GGCACGTGGC
 CTTCTTCAAC TTGATGGCC TGGACGAGCT GCACCTGGAC TTGGACCTCA GCGCGCTGCC
 TACAGCTCC TGGCCTGGG AGCCTGCCCA GCGCCTGGTC TTGCTGGCCA ACCTGCTCAG
 TGGAAAGCTG CTGAAGGGGG CTAGCAAGCT GCTCAGAGCC GGCACAGGCA TGGAGGTGCC
 GCGCCAGTTC CTGCGGAAGA AGGTGCTTCT CCGGGGCTTC TCCCCAGCC ACCTSCGCGC
 CTATGCCAGG AGGATGTTCC CCGAGCGGCG CTTGCAGGAC CGCCTGCTCA GCCAGCTTGA
 GGCCAAACCC AACCTCTTCA GCCTGTGCTC TGTGCCCCCTC TTCTGCTGGA TCATCTTCCG
 GTGCTTCCAG CACTTCCCTG CTGCTTTTCA AGGCTCAGCA CAGCTGCCCC ACTGCACGAT
 GACCTGACA GATGTCTTCC TCTGCTCAC TTAGGTCCAT CTGAACAGGA TGCAGCCGAG
 CAGCCTGCTG CAGCGGAACA CACCGAGCCC AGTGGAGACC CTCCAGCCCG GCGGGGACAC
 TCTGTGCTCG CTGGGGCAGG TGGCCACCG GGGCATGGAG AAGAGCCTCT TTGTCTTCCG
 CAGGAGGAG GTGCAGGCTT CCGGGCTTCA GGAGAGAGAC ATGCAGCTGG GCTTCTCTCG
 GGTCTTCCCG GAGCTGGGCC CCGGGGTGA CAGCAGTCC TATGAGTTTT TGCACCTCAG
 TCTCAGGCC TTCTTTACAG CTTCTTCTCT GCTGCTGGAC GACAGGGTGG GCACCTCAGGA
 CTTCTCAGG TTCTTCCAGG AGTGGATGCC CCTTCCGGGG GCAGCGACCA CTTCTCTCTA

FIG. 3 (page 1 of 2)

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TCTTCGCTTC CTCCGCTTCC AGTGGCTGCA GGGCAGTGGT CCGCGCGCGG AAGACCTCTT
 TAAGAACAAG GATCACTTCC AGTTACCAAA CTTCTTCTCT TCGGGGCTGT TGTCCAAAGC
 TAAACAGAAA CTCTTCCGGC ATCTGCTGCC CCGCGCAGCC CTCAGGAGAA AGCGCAAGGC
 TCTGTGGGCA CACCTGTTTT CCAAGCCTCC GGGCTACCTG AAGAGCCTCC CCGCGCTTCA
 TGTGAAAGC TTCAACCAAG TCAAGGCCAT CCGCAGCTTC ATCTGGATGC TCGGCTTCAT
 TTACGAGACA CAGAGCCAGA AGGTGGGGCA GCTGGCGCGC AGGGGCATCT GCGCCAACTA
 TCTCAAGCTG ACCTACTGCA ACCTCTCTCT GCGCCACTGC AGCGCCCTCT CTTTCTCTCT
 GCATCACTTC CCGAAGCGGC TCGCCCTAGA CCTAGACAAC AACATCTCA ACGACTACGG
 CCGTGGGGAG CTGCAGCCCT GCTTCAGCCC CCTCACTGTT CTCAGACTCA GCGTAAACCA
 GATCACTGAC GGTGGGGTAA AGGTGCTAAG CCAAGAGCTG ACCAAATACA AAATTGTGAC
 CTATTGGGT TTATACAACA ACCAGATCAC CCAATGTGGA GCGAGGTACG TCACCAAAAT
 TCTGGATCAA TCAAAAGGCC TCAAGCATCT TAACTGGA AAAACAAAA TAACAAGTCA
 AGGAGGGAAG TATCTGCCCC TCGCTGTGAA GAACAGCAAA TCAATCTCTG AGGTGGGAT
 GTGGGGCAAT CAAGTTGGGG ATGAAGGAGC AAAAGCCTTC GCAGAGGCTG TCGGGAACCA
 CCCCAGCTTC ACCACCCCTCA GTCTTCTCTC CAACGGCATC TCCACAGAAG GAGGAAAGAG
 CTTTGGGAGG GCGCTGCAGC AGAACAGCTC TCTAGAAATA CTGTGGCTCA CCGAAATCA
 ACTCAACGAT CAAGTGGCAG AGAGTTTGGC AGAAATGTTG AAAGTCAACC AGACGTTAAA
 GCATTTATGG CTTATCCAGA ATCAGATCAC AGCTAAGGGG ACTGCCCCAGC TCGCAGATGC
 GTTACAGAGC AACACTGGCA TAACAGAGAT TTGCTTAAAT GGAAACCTCA TAAACCAGA
 TGAGGCCAAA GTCTATGAAG ATGAGAAGCG GATTATCTCT TTCTGAGAGG ATGCTTTCTT
 TTCTATGGGG TTTTGGCCCT CGAGCCTGAG CAGCAAAATGC CACTCTGGGC AGTCTTTTCT
 TCAAGTGTCT TAAAGGGGGC TCGCGAGGCG GCACTATCAG GAGTCCACTG CCTTCATGAT
 GCAAGCCAGC TTCTGTGCA GAAGGTCTCG TCGGCAAACT CCTAAGTAC CCGCTACAAT
 TCTGCAGAAA AAGAATGTGT CTTTCCAGCT GTTGTAGTTA CAGTAAATAC ACTGTGAAGA
 GAAAAAAAA ACGGACGCGT GG (SEQ ID NO:7)

FIG. 3 (page 2 of 2)

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MEEQCHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAEIWCACFTQP
CKVRKILLVQSKGZEEVSEFFLWLLQQLADAYVDLRFWLLLEIGFSPSLLTQSKVVVNTDFVSRYT
QQLRHHLCGRDSKFVLCYAKKEELLLEETVMDTIMELVGFSNESLGSLSNSLACLDDHTTGTILNEQG
ETIFELGDAGVGKSMILLQRLQSLNATGRLEDAGVKFFTHFRCRMFSCTKESDRLCLQDLLFKHYCY
PERDPHEVTAFLLRFPFWALFTFDGLDELHSDLDLSRVPDSSCFWEPAPLVLNLLSGKLLKG
ASKLLTARTGIEVPROFLRKKVLLRGFSPSHLRAYARRMFPERALQDRLLSQLEANPNLCSLCSV
PLFCNIIIFRCFQHFRAAFEGSFQLPDCTMTLTVDVLLVTEVHLNRMQPSSLVQRNTRSPVETLHA
GRDTLCSLGQVAHRGMEKSLFVFTQEEVQASGLQERDMQLGFLRALFELGPGGDQQSYEFFHLTL
QAFFTAFFLVLDDEVGTQELLRFFQEWMPFAGAATTSCYPPFLPFQCLQGSGPAREDLFKNKDH
QFTNLFLCGLLSKAKQKLLHLLVFAAALRRKRKALNAHLFSSLRGYLKSLPRVQVESFNQVQAMP
TFIWMLRCTIYETQSQKVGQLAARGICANYLKLTYCNACSADECSALSFLVHHFPKRLALDLENNNL
NDYGVRELQPCFSRLTVLRLSVNQITDGGVKVLSEELTKYKIVTYLGLYNNQITDVGARYVTKIL
DECKGLTHLKLKGNKITSEGGKYLALAVKNSKSISEVGMWGNQVGDEGAKAFEAALRNHPSLTTL
SLASNGISTEGGKSLARALQQNTSLEILNLTQNELNDEVAESLAEMLKVNQTLKHLWLIQNQITA
KGTAQLADALQSNTGITEICLNGNLINPFEAKVYEDEKRIICF (SEQ ID NO:8)

FIG. 4

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09729721.120100

TACGGCTCCSACTTCTGAGAAATGACTACTTCTCGGCCAAGATGCGGAGATTSTGT
TTCCTTSCCCCAACCCAGCCTGACAAAGGTCCSCAAAATTCTGACCTGGTACAGAGCAAG
TCCGAGGAGGTGTCCGAGTTCTTCTCTACTTCTCTCAGCACTCCGAGATGCCCTACGT
TGACCTCAGGCCCTTSGGCTGCTGAGATCGGCTTCTCCCTTCCCTGCTCACTCAGAGCA
AAGTCTGGTCAACACTGACCCAGTGAGCAGGTATACCCAGCAGCTGCGACACCATCTG
TCCCTGACTGCAAGTTCTGCTGCTGCTATGCCCAAGAGGAGGAGCTGCTGCTGAGGA
TATCTACATGGACACCATCATGGAGCTGGTTGGCTTCAGCAATGAGAGCCTGGGCAGCC
TGAACAGCCTGGCCTGCTCTGACCCACACCACCGGCATCTCAATGAGCAGGGTGAG
ACCATCTTCATCCTGGGTGATGCTGGGTGGGCAAGTCCATGCTGCTACAGCGGCTGCA
TAGCCTCTGGGCCACGGGCCGGCTAGACGCAGGGGTCAAATTCTTCTTCCACTTTCGCT
TCCGCATGTTTCAGCTGCTTCAAGGAAAGTGACAGGCTGTGTCTGCAGGACCTGCTCTTC
AAGCACTACTGCTACCCAGAGCGGGACCCCGAGGAGGTGTTTGCCTTCTGCTGCGCTT
CCCCCAGCTGGCCCTCTTCACTTTCGATGGCCTGGACGAGCTGCACTCGGACTTGGACC
TGAGCCGCGTGCTGACAGCTCTTGGCCCTGGGAGCCTGCCACCCCTGGTCTTGTCTG
GCCAACCTGCTCAGTGGGAAGCTGCTCAAGGGGGCTAGCAAGCTGCTCACAGCCCGCAC
AGGCATCGAGGTCCCGCGCCAGTTCTGCGGAAGAAGGTGCTTCTCCGGGGCTTCTCCC
TCAGCCACCTGCGCGCCTATGCCAGGAGGATGTTCCCGGAGCGGGCCCTGCAGGACCCG
TTGCTGAGCCAGCTGGAGGCCAACCCCAACCTCTGCAGCCTGTGCTCTGTGCCCTCTT
TTGCTGGATCATCTTCCGGTGTCTTCAGCACTTCCGTGCTGCCCTTTGAAGGCTCACAC
AGCTGCCCSACTGCACGATGACCTGACAGATGTCTTCTCTCTGGTCACTGAGGTCCAT
CTGAACAGGATGCAGCCCAGCAGCCTGCTGCAGCGGAACACACGCAGCCAGTGGAGAC
CTTCCACGCGCGGACACTCTGTGCTGCTGGGGCAGGTGGCCACCGGGGCATGG
AGAAGAGCCTCTTTGTCTTCAACAGGAGGAGGTGCAGGCCCTCCGGGCTGCAGGAGAGA
GACATGCAGCTGGGCTTCTTCCGGGCTTTGCCGGAGCTGGGCCCCGGGGGTGACCAGCA
GTCTATGAGTTTTTCCACCTCAGCCTCCTCACCTGTAAAACTGGGATCCAGTATAGA
CTTTGGAATCAGTAGACACCATATGCTTCAAAAAACAGGGGCTATTAAAAATGACATCA
GGAGCCAGAAAGTCTCATGGCTGTGCTTTCTCTTGAAGTTTATACAACAACAGATCAC
CGATGTCCGAGGCCAGACTGGGAAAAAATAAACAAGTGAAGGAGGGAAGTATCTCG
CCCTGGCTGTGAAGAACAGCAAATCAATCTCTGAGGTTGGGATGTGGGGCAATCAAGTT
GGGGATGAAGGAGCAAAGCCTTCCAGAGGCTCTGCGGAACCACCCCAGCTTGACCAC
CCTGAGTCTTGCGTCCAACGGCATCTCCACAGAAGGAGGAAAGAGCCTTGGAGGGGCC
TGACGCAGAACACGTCTCTAGAAATACTGTGGCTGACCCAAAATGAATCAACGATGAA
TTGGCAGAGAGTTTGGCAGAAATGTTCAAGTCAACCAGACGTTAAAGCATTTATGGCT
TATCCAGAATCAGATCACAGTCTTTTTGTGTGAGTGTCTTAAAGGGGCTTCCGAGGGCG
GACTATCAGGAGTCCACTGCCCTCATGATGCAAGCCAGCTTCTCTGTGCAGAAAGTCTGG
TCGGCAAACCTCCCTAAGTACCCGCTACAATTCTGCAGAAAAAGAATGTGTCTTGGCAGC
TGTTGTAGTTACAGTAAATACACTGTGAAGAGACTTTATTGCCTATTATAATTATTTT
ATCTGAAGCTAGAGGAATAAAGCTGTGAGCAAACAGAGGAGGCCAGCCTCACCTCATT
CAACACCTGCCATAGGGACCAACGGGAGCGAGTTGGTCACCGCTCTTTTCATTGAAGAG
TTGAGGATGTGGCACAAGTTGGTGCCAAGCTTCTTGAATAAAACGTGTTTGATGGATT
AGTATTATACCTGAAATATTTTCTTCTCTCAGCACTTTCCCATGTATTGATACTGGT
CCCACTTCACAGCTGGAGACACCGAGTATGTGCAGTGTGGGATTTGACTCCTCAAGG
TTTTGTGGAAAGTTAATGTCAAGGAAAGGATGCACCACGGGCTTTTAATTTTAATCCTG
GAGTCTCACTGTCTGCTGGCAAAGATAGAGAATGCCCTCAGCTCTTAGCTGGTCTAAGA
ATGACGATGCCCTTCAAAATGCTGCTTCCACTCAGGGCTTCTCCTCTGCTAGGCTACCT
CCTCTAGAAGGCTGAGTACCATGGGCTACAGTGTCTGGCCTTGGGAAGAAGTGATTCTG
TCCCTCCAAAGAAATAGGGCATGGCTTGGCCCTGTGGCCCTGGCATCCAAATGGCTGCT
TTGTCTCCCTTACCTCGTGAAGAGGGGAAGTCTTCTCTGCTGCCCTCCCAAGCAGCTGAAG
GGTGAATAAACGGGGCGCAAGACTCAGGGGATCGGCTGGGAACCTGGGCCAGCAGAGCAT
TTTGGACACCCCCCACCATGGTGGGCTTGTGGTGGCTCTCCATGAGGGTGGGGGTGAT
ACTACTAGATCACTTGTCTCTTGGCAGCTCATTTGTTAATAAAATACTGAAACACAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA (SEQ ID NO:25)

FIG. 5

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RASDLLKNDYFSAEDAEIWCACFTQPKVRKILLVQSKGEZVSEFFLYLL
QQLADAYVDLRPWLLLEIGFSPSLITQSKVWNTDPVSRYTQQLRHHLGRDS
KFVLCYAOKEELLLEETIMDTIMELVGFSNESLGSLSLACLLDHTTGILN
EQGETIFILGDAGVGKSMILLCRLQSLWATGRLDAGVKFFHFRCRMFSCFK
ESDRCLQDILLFKHYCYPERDPEEWFALRLRFPHVAFETFDGLDELHSDLD
LSRVPDSSCPWEPAPPLVLLANLLSGKLLKGASKLLTARTGIEVPROFLRK
KVLRLGFSFPHLRAYARRMFPERALQDRLLSQLEANPNLCSLCSVPLFCWI
IFRCFQHFRAAFEGSPQLPDCITLITDVFLLVTEVHLNRMQPSSLVQRNTR
SPVETLHAGRDTLCSLGQVAHRCMEKSLFVFTQEEVQASGLQERDMQLGFL
RALFELGPGGDQQSYEFFHLSLLTCKTGIFV (SEQ ID NO:26)

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FIG. 6

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	10	20	30	40								
1	EEHGH	LLKH	THIRNTQ	NDY	CARD4-CARD							
2	QGGIAC	WQKEDIN	INQS	SRDL	CARD3-CARD							
3	ACSR	PSETHDRE	KRL	ETQADSG	ARC-CARD							
4	KACDE	SLLKH	MFR	VE	CARD1-CARD							
5	KESNDIL	RIIKHE	MALFHL	VIS	CARD2-CARD							
	50	60	70	80								
15	FSALDAE	ICCE	QDKN	KILLL	SEEVSEFFYL	CARD4-CARD						
19	IMEDY	LLST	RTSK	QL	ITDIQ	EFKIVQK	CARD3-CARD					
27	LTGPEY	ALD	LDERR	RLILL	G	CCQLR	ARC-CARD					
35	YH	QD	DI	QITQ	IL	AB	I	IN	NIE	KNG	CARD1-CARD	
36	ITEQ	EDVI	Q	TQTS	LA	BE	I	IL	NIA	TRE	RS	CARD2-CARD
	90	100										
75	EQLE	DEYVD	REW	EIGF	ELL							CARD4-CARD
79	EKDNKQ	MG	Q	PEI	VVS	RS						CARD3-CARD
77	ART	G	POPA	WDNQ	VG							ARC-CARD
75	EKE	IDST	KN									CARD1-CARD
76	AEAVI	EHI										CARD2-CARD

0073074 120400

FIG. 7

00720721-120400

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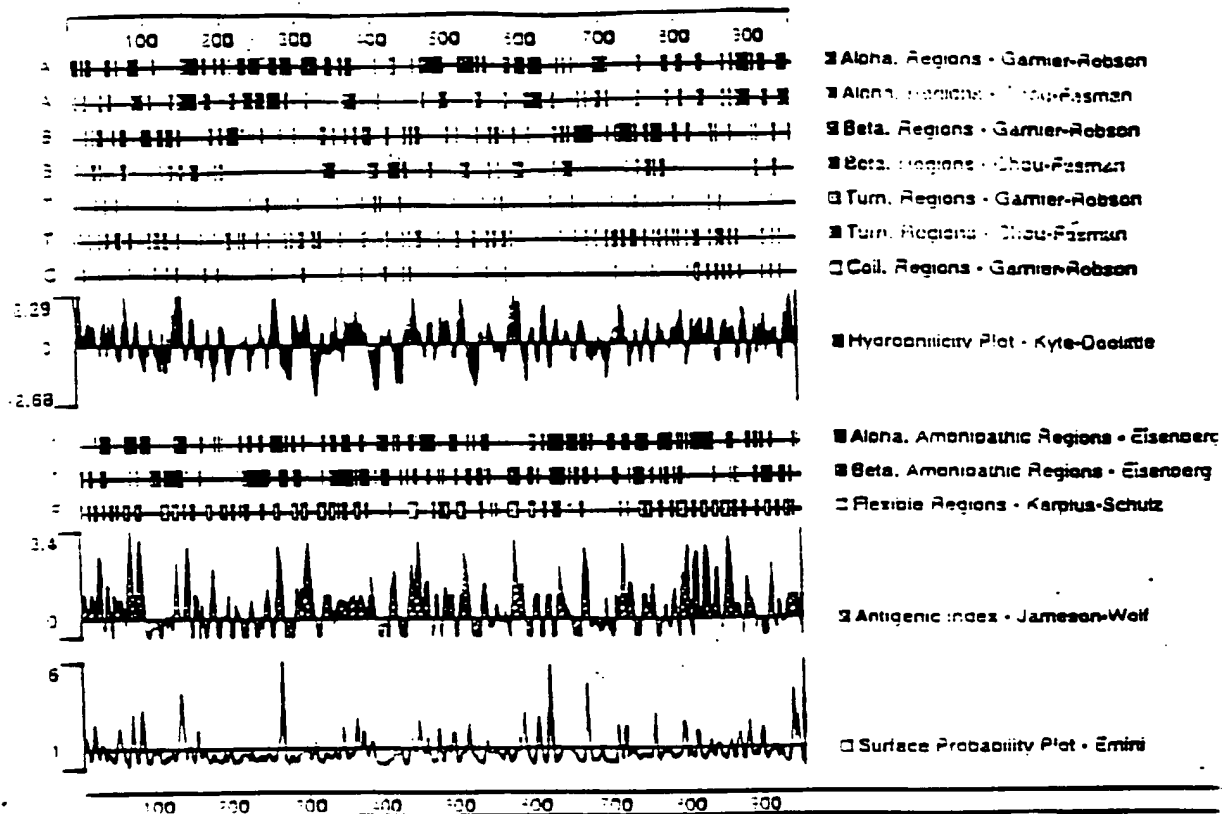


FIG. 8

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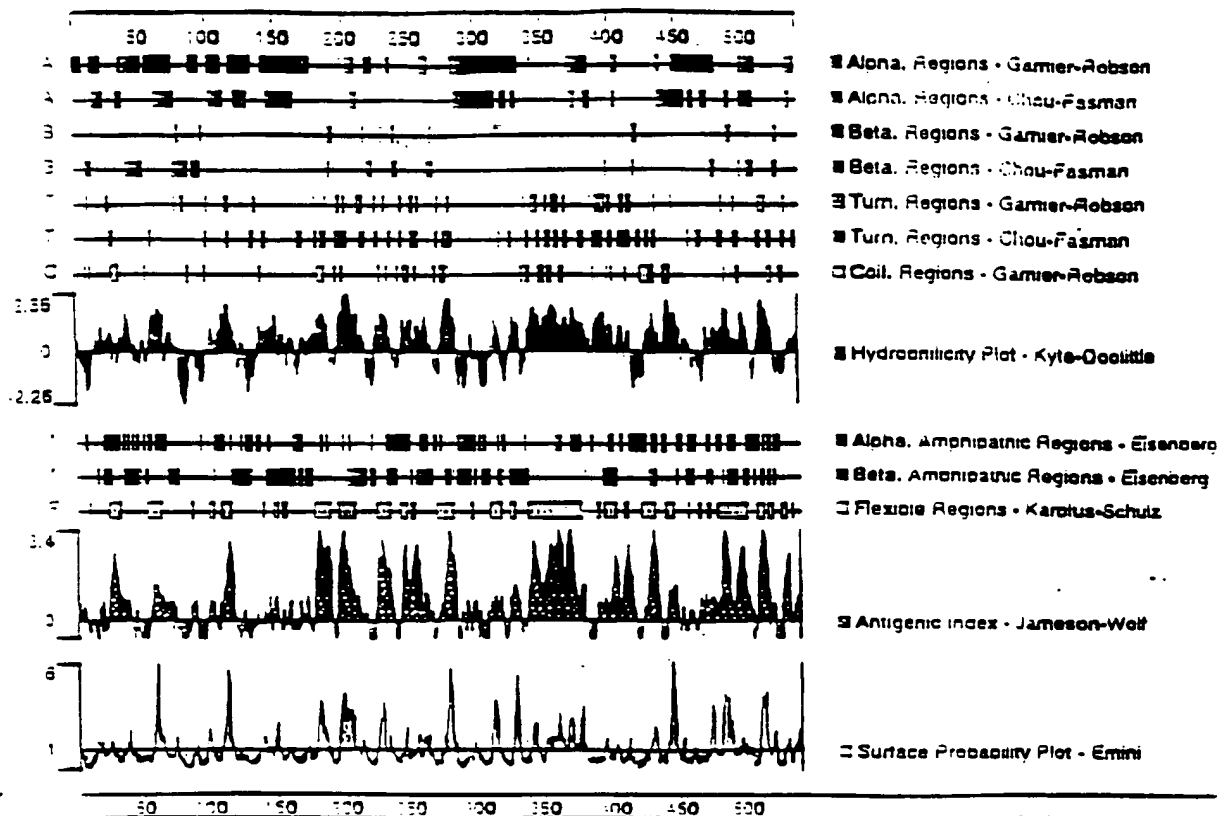


FIG. 9

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 213. **Figure 203**
 214. **Figure 204**
 215. **Figure 205**
 216. **Figure 206**
 217. **Figure 207**
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FIG. 10 (Page 1 of 3)

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CCAGGCCTTCTTTACAGCCTTCTTCTCTGCTGGACGACAGGGTGGGCACCTCAGGAGCT
GCTCAGGTTCTTCCAGGAGTGGATGCCCCCTGCGGGGGCAGCGACCAAGTCTTCTATCC
TCCCTTCTTCCCGTTCCAGTGCCTGCAGGGCAGTGGTCCCGCGCGGAAGACCTCTTCAA
GAACAAGGATCACTTCCAGTTCAACCAACCTCTTCTGTGCGGGCTGTTGKCCAAAGCCAA
ACAGAAACTCTGCGGCATCTGGTGGCCGCGGCAGCCCTGAGGAGAAAGCGCAAGGCCCT
GTGGGCACACCTGTTTTCCAGCCTGCGGGGCTACCTGAAGAGCCTGCCCCGCGTTCAGGT
CGAAAGCTTCAACCAGGTGCAGGCCATGCCACGTTTCTGATGCTGCGGTGCATCTA
CGAGACACAGAGCCAGAAGGTGGGGCAGCTGGCGGCCAGGGGCATCTGCGCCAACCTACCT
CAAGCTGACCTACTGCAACGCCTGCTCGGCCGACTGCAGCGCCCTCTCTTCTGCTCTGCA
TCACTTCCCCAAGCGGCTGGCCCTAGACCTAGACAACAACAATCTCAACGACTACGGCGT
GCGGGAGCTGCAGCCCTGCTTCAGCCGCTCACTGTTCTCAGACTCAGCGTAAACCAGAT
CACTGACGGTGGGGTAAAGGTGCTAAGCGAAGAGCTGACCAAATACAAAATTGTGACCTA
TTTGGGTTTATACAACAACCAGATCACCGATGTGCGAGCCAGGTACGTCAACCAAATCCT
GGATGAATGCAAAGGCCTCAGCATCTTAAACTGGGAAAAAACAAAATAACAGTGAAGG
AGGGAAGTATCTCGCCCTGGCTGTGAAGAACAGCAAATCAATCTCTGAGGTGGGATGTG
GGGCAATCAAGTTGGGGATGAAGGAGCAAAAGCCTTCGCAGAGGCTCTGCGGAACCAACC
CAGCTTGACCACCCTGAGTCTTGGCTCCAACGGCATCTCCACAGAAGGAGGAAAGAGCCT
TGCGAGGGCCCTGCAGCAGAACACGTCTCTAGAAATACTGTGGCTGACCCAAAATGAACT
CAACGATGAAGTGGCAGAGAGTTTGGCAGAAATGTTGAAAGTCAACCAGACGTTAAAGCA
TTTATGGCTTATCCAGAATCASATCACAGCTWARGGACTGCCCAGCTGGCAGATGCGTT
ACAGAGCAACACTGGCATAACAGAGATTTGCCTAAATGGAAACCTGATAAAACCAGAGGA
GGCCAAAGTCTATGAAGATCAGAAGCGGATTATCTGTTTCTGAGAGGATGCTTCTCTGTT
CATGGGGTTTTTGGCCCTGGAGCCTCAGCAGCAAATGCCACTYTGGGCAGTCTTTTGTGTC
AGTGTCTTAAAGGGGCTGCGCAGGCGGGACTATCAGGAGTCCACTGGCTCCATGATGCA
AGCCAGCTTCTCTGTGCAGAAGGTCTGGTGGGCAAACTCCCTAAGTACCCGCTACAATTCT
GCAGAAAAAGAATGTGTCTTGGCAGCTGTTGTAGTTACAGTAAATACACTGTGAAGAGAC
TTTATTGCCTATTATAATTATTTTTATCTGAAGCTAGAGGAATAAAGCTGTGAGCAAACA
GAGGAGGCCAGCCTCACCTCATTCCAACACCTGCCATAGGGACCAACGGGAGCGAGTTGG
TCACCGCTCTTTTCATTGAAGAGTTGAGGATGTGGCACAAGTTGGTGCCAAGCTTCTTG
AATAAAACGTGTTTGTGATTAGTATTATACCTGAAATATTTTCTTCTCTCAGCACT
TTCCCATGTATTGATACTGGTCCCCTTCAACAGCTGGAGACACCGGAGTATGTGCAGTGT
GGGATTGACTCCTCCAAGGTTTTGTGGAAAGTTAATGTCAAGGAAAGGATGCACCACGG

FIG. 10 (Page 2 of 3)

GCTTTTAATTTTAATCCTGGAGTCTCACTGTCTGCTGGCAAAGATAGAGAATGCCCTCAG
CTCTTAGCTGGTCTAAGAATGACGATGCCTTCAAAATGCTGCTTCCACTCAGGGCTTCTC
CTCTGCTAGGCTACCCCTCCTCTAGAAGGCTCAGTACCATGGGCTACAGTGTCTGGCCTTG
GGAAGAAGTGATTCTGTCCCTCCAAAGAAATAGGGCATGGCTTGCCCCCTGTGGCCCTGGC
ATCCAAATGGCTGCTTTTGTCTCCCTTACCTCGTGAAGAGGGGAAGTCTCTTCCTGCCTC
CCAAGCAGCTGAAGGGTGACTAAACGGGCGCCAAGACTCAGGGGATCGGCTGGGAAGTGG
GCCAGCAGAGCATGTTGGACACCCCCCACCATGGTGGGCTTGTGGTGGCTGCTCCATGAG
GGTGGGGGTGATACTACTAGATCACTTGTCTCTTGGCAGCTCATTGTTAATAAAATAC
TGAAAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGG (SEQ ID NO:38)

FIG. 10 (Page 3 of 3)

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MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAEIVCA
CPTQPKVRKILDLVQSKGEEVSEFFLYLLQQLADAYVDLRFWLLEIGFSPSLLTQSKVV
VNTDPVSRYTQQLRHHLGKDSKFVLCYAKKEELLLEEIYMDTIMELVGFSNESLGSLNSL
ACLLDHTTGILNEQAASRKVTGCVCRSCSSSTTATQSGTFRRCCLPSCCASPTWPSSPSMA
WTSCTRIWT (SEQ ID NO:39)

FIG. 11

007287.21.120400

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CACGCGTCCGCGCTACTSCGGGAGCAGCGTCTCTCCCGGGCCACGGCGCTTCCCGGCCCCG
GCGTCCCCCGGACCATGGCGCTCTCCCGGCTCTTCTCTAGCTCTCAGCGGCTGCGAAGTCT
GTAAACCTSGTGCCCAAGTGATTSTAGTCAGGAGACTTTCTTCCGTTTCTGCCTTTGA
TGGCAAGAGGTGGAGATTSTGGCGGCGATTACAGAAAACATCTGGGAAGACAAGTTGCTG
TTTTTATGGGAATCGCAGGCTTGGGAAGAGACAGAAGCAATTCAGAAATAAATTGGAAAT
TGAAGATTTAAACAATGTTGTTTTTAAATATTCTAACTTCAAAGAATGATGCCAGAACT
TAAAAAGGGGCTGCGCAGAGTAGCAGGGGCCCCCTGAGGGGCGGGCCCTGAATCCTGATTGC
CCTTCTGCTGAGAGGACACACGCAGCTGAAGATGAATTTGGGAAAAGTAGCCGCTTGCTA
CTTTAACTATGGAAGAGCAGGGCCACAGTGAGATGGAAATAATCCCATCAGAGTCTCACC
CCCACATTCAATTACTGAAAAGCAATCGGGAACCTTCTGGTCACTCACATCCGCAATACTC
AGTGTCTGGTGGACAACCTTGTCTGAAGAATGACTACTTCTCGGCCGAAGATGCGGAGATTG
TGTGTGCTGCCCCACCCAGCCTGACAAGGTCCSCAAAATTCTGGACCTGGTACAGAGCA
AGGGCGAGGAGGTGTCCGAGTTCTTCTCTACTTGCTCCAGCAACTCCAGATGCCTACG
TGGACCTCAGGCCTTGGCTGCTGGAGATCGGCTTCTCCCCCTTCCCTGCTCACTCAGAGCA
AAGTCGTGGTCAACACTGACCCAGGTAGGAGTCAGCCCCAGCAAGACCGCAGGCACCACT
GCAAGCAGGGCCCCCTGGGGGGTTTGGTAATGGCTGGGCCAGCCCTGAGTGCCACCTCAGGA
AGCAGGGCCCAGGTGCTATTTTGATTTTAGAAAGGAACAGCTGAATCCTGTCTCCCAAGTG
CAGCCCAGGTGGCTGCGATTGAACTGCCCCACACCTCGATGGTCTGGTTTATAGAGGGGCC
TTTGGAAGTATGGGAATGGCCTGTGTTCTGACCCCTTGCTTTCTTCTTCTGACATAT
GTAGACATTTTAATGGTTGCACAAATTCAAGGTTGTATTTTTTTTTCTTTAAAAAAATCT
TTAGCTGGACATGGTAGCACACACCTGTAGTTCCAGCTACTCAGGAGGCTGAGGCAAGAG
TACTGCTTGAGCCCCAGAGTCTAAGGCTGCAGCGAGCTATGATTGTGCCCCCTACACTCCA
CAGCCTGGGTTTTAGAGTGAGACCCTGTCTCTAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAANGGGCGG (SEQ ID NO:40)

FIG. 12

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MEEQGHSEMEIIPSESHPHIQLLXSNRELLVTHIRNTQCLVDNLLKNDYFSAEDAEIVCA
CPTQPDKVRKILDLVQSKGEEVSEFFLYLLQQLADAYVDLRFWLLEIGFSPSLLTQSKVV
VNTDFGRSQFQQDRRHQCKQGFGGSGNGWASPECHLRKQAQVLF
(SEQ ID NO:41)

FIG. 13

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00720724 130400

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	MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCL	Majority
	10 20 30 40	
1	MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCL	CARD4-Y CLONE
1	MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCL	CARD4-Z CLONE
1	MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCL	CARD4L
	VDNLLKNDYFSAEDAEIVCACPTQPKVRKILDLVOSKGE	Majority
	50 60 70 80	
1	VDNLLKNDYFSAEDAEIVCACPTQPKVRKILDLVOSKGE	CARD4-Y CLONE
1	VDNLLKNDYFSAEDAEIVCACPTQPKVRKILDLVOSKGE	CARD4-Z CLONE
1	VDNLLKNDYFSAEDAEIVCACPTQPKVRKILDLVOSKGE	CARD4L
	EVSEFFLYLLOQLADAYVDLRPWLLEIGFSPSLLTOSKVV	Majority
	90 100 110 120	
1	EVSEFFLYLLOQLADAYVDLRPWLLEIGFSPSLLTOSKVV	CARD4-Y CLONE
1	EVSEFFLYLLOQLADAYVDLRPWLLEIGFSPSLLTOSKVV	CARD4-Z CLONE
1	EVSEFFLYLLOQLADAYVDLRPWLLEIGFSPSLLTOSKVV	CARD4L
	VNTDPVSRYTQOLRHHLGGRDSKFVLCYAOKEELLLEEIYM	Majority
	130 140 150 160	
121	VNTDPVSRYTQOLRHHLGGRDSKFVLCYAOKEELLLEEIYM	CARD4-Y CLONE
121	VNTDPGRSOPQQDRRI	CARD4-Z CLONE
121	VNTDPVSRYTQOLRHHLGGRDSKFVLCYAOKEELLLEEIYM	CARD4L
	DTIMELVGFSNESLGSLSLACLDDHTTGILNEOXXXX -	Majority
	170 180 190 200	
161	DTIMELVGFSNESLGSLSLACLDDHTTGILNEOAAASR -	CARD4-Y CLONE
137	DTIMELVGFSNESLGSLSLACLDDHTTGILNEOAAASR -	CARD4-Z CLONE
161	DTIMELVGFSNESLGSLSLACLDDHTTGILNEOGETIFI	CARD4L
	-----XCXXXX	Majority
	210 220 230 240	
199	-----FVTVG	CARD4-Y CLONE
137	-----QCEQ	CARD4-Z CLONE
201	LG DAGVGKSM L L QRLQSLWATGR LDAGVKFFHFRCGRMFS	CARD4L
	-----XC-----	Majority
	250 260 270 280	
203	G-----V	CARD4-Y CLONE
141	-----	CARD4-Z CLONE
241	GFKESDRLGLQD L L FKH YCYPERDPEEVFAFLLRFP HVAL	CARD4L
	-----KXCKXX-----	Majority
	290 300 310 320	
106	-----RTGSSS-----	CARD4-Y CLONE
141	-----	CARD4-Z CLONE
281	FTFDGLDELHSDLDLSRVDDSSGPWEPAPHPVLLANLLSG	CARD4L

FIGURE 14 (1 of 4)

Questions are asked from both sides of the road.

FIGURE 14 (2 of 4)

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-----KKPKKKW-----				Majority
	650	660	670	680
133	-----SSPSMAW-----			CARD4-Y CLONE
133	-----SSPSMAW-----			CARD4-Z CLONE
641	IEFNQVQAMPTFTWMLRCITETQSQKVGQLAARGICANYL			CARDAL
-----KKCKXX-----				Majority
	690	700	710	720
142	-----TSTRT-----			CARD4-Y CLONE
133	-----TSTRT-----			CARD4-Z CLONE
651	KLTVCNAQSADCSALSFLVLRHFPRLALDLDNNNLNDYGV			CARDAL
-----				Majority
	730	740	750	760
148	-----			CARD4-Y CLONE
133	-----			CARD4-Z CLONE
711	RELQPCPSRLTVLRLSNQITDGGVXVLSSEELTKYKITY			CARDAL
-----ECK-----				Majority
	770	780	790	800
148	-----			CARD4-Y CLONE
133	-----			CARD4-Z CLONE
761	LGLYNNQITDVGARYTKILD ECKGLTHLSLYNNQITDVG			CARDAL
-----WXXXXXXXXX-----				Majority
	810	820	830	840
148	-----			CARD4-Y CLONE
133	-----			CARD4-Z CLONE
801	ARLGKNKITSEGGKYLALAVHNSKKSISEVGMWGNQVGDEG			CARDAL
XXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX				Majority
	850	860	870	880
149	-----			CARD4-Y CLONE
133	-----			CARD4-Z CLONE
841	AKAFAEAIPNHPSLTTLASNGISTEGGKSLARALQQNT			CARDAL
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX				Majority
	890	900	910	920
149	-----			CARD4-Y CLONE
133	-----			CARD4-Z CLONE
851	SLCETIWLCQNEELNDEVAESLAEMLVNQTLKHLWLIQNQI			CARDAL
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX				Majority
	930	940	950	960
149	-----			CARD4-Y CLONE
133	-----			CARD4-Z CLONE
911	TAKSTAGLADALQSNTEITELCNGNLKPEEAKVYEDEK			CARDAL

FIGURE 14 (3 of 4)

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XXXXF					Majority
149					
154	-	-	-	F	CARD4-Y CLONE
161	E	-	-	F	CARD4-Z CLONE
					CARD4L

Decorations: Decorations 11: Shade (with solid black) residues that match the Consensus exactly.

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007074-1000
007074-1000

CCACGCGTCCGCGGACCCGCGAGCGGTAGCGCCCTCCCTCCCAGCTGTTGTCCGCGCCGAT
CCGCGACCCCTAGTCCCCGATCCGCTTCTGAGAGTCACCGTACTCCAGGGCCAACTGAG
CCAAAGTCCCTGCCAACTTGGGTGAGCAATGAAAGGCAGGATCCTGGGTGGTGGCCCTGAA
TCTGATTTGTCTGCGCTGCCAGCGAGACACATGTGGTCAAAGATGAATTTGAGAAAAGT
AGCTGCTGGCTACTTGAACAATGGAGGAACACGGCCATCATGAGATGGAAGGCACCCCAT
TGGGTGTGCACTCCACATTAAGTCTGGAAGATCAACAGGGAACATCTGGTCACCAACA
TTCGGAACACTCAGTGTCTGCTGGACAACCTTGTCTGGAGAATGGCTACTTCTCAGCCGAAG
ATGCAGAGATTGTGTGTGCTTCTCCCAACCAAGCCTGACAAGGTCCGAAAGATCCTTGACC
TGGTGCAGAGCAAAGGCGAGGAGGTGTCTGAGTTCTTCTCTACGTGCTGCAGCAGCTGG
AGGATGCTTACGTGGACCTCAGGCTGTGGCTCTCAGAAATTGGCTTCTCCGCTTCCCAGC
TCATTCCGACCAAACTATCTCAATACTGACCCAGTAAGCAGGTATACCCAACAGCTGC
CACACCAACTGGGCGCGACTCCAAGTTCATGCTGTGCTACGCCCAGAAGGAGGACCTGC
TGCTGGAGGAGACCTATATGGACACACTCATGGGGCTSGTAGGCTTCAACAATGAAAACC
TGGGCAGCCTAGGAGGCCTGATTGCTTCTGGACCACAGTACGGGCGTCTCTAACGAGC
ATGGCGAGACTGTCTTCTGTGTCTGGGGACGCGGAGTGGGCAAGTCCATGCTGCTGCAGA
GGTTGCAGAGCCTCTGGGCGTCAGGCAGGTTGACCTCCACAGCCAAATTCTTCTTCCACT
TCCGCTGCCGATGTTTCTGCTGCTTCAAGGAGAGCGACATGCTGAGTCTGCAGGACCTGC
TCTTCAAGCATTCTGCTACCCGAGCAGGACCCCGAGGAGGTGTTCTCCTTCTTGTCTGC
GCTTTCGCCACACAGCGCTCTTCACTTTTGACGGCCTGGATGAGCTGCACTCAGACTTCG
ACCTGAGCCGCGTGGCGGATAGCTGCTGCCCCCTGGGAGCCGGCTCACCCCTCTGGTCTCTGC
TGGCTAACCTCCTAAGTGGGAGGCTGCTCAAGGGTGGCGGCAAATTGCTCACTGCTGCGCA
CAGGCGTGGAGGTCCCCCGCCAGCTCCTGCGCAAAAAGGTGCTGCTCCGCGGCTTCTCCC
CAAGTCACCTGCGCGCTATGCCCCCGGATGTTCCCCGAGCGCACAGCGCAGGAGCATC
TGCTGCAGCAGCTGGATGCCAACCCTAACCCTCTGCAGCCTGTGCGGGGTGCCGCTCTTCT
GTTGGATCATCTTCCGTTGTTTCCAGCACTTCCAGACGGTCTTCGAGGGCTCCTCTTCAC
AGTTGCCGGACTGTGCTGTGACCCTGACCGATGTCTTTCTGCTGGTCACTGAGGTGCATC
TGAACAGGCCGCGAGCCGAGCAGCCTGGTGCAGCGCAACACGCGCAGCCCGGCGGAAACCC
TACGTGCAGGCTGGCGCACGCTGCATGCGCTGGGAGAGGTGGCTCACCGAGGCACCCACA
AGAGCCTCTTTGTGTTTGGCCAGGAGGAGGTGCAGGCGTCAAGCTGCAGGAAGGAGATC
TGCAGCTGGGCTTCTGCGGGCTTTGCCCGATGTGGGCGCTGAGCAGGGCCAGTCTTACG
AATTTTCCACCTTACGCTCCAGGCCTTCTTCAACGCTTCTTCTCTGGTAGCAGATGACA
AAGTGAGCACCCGGGAGTTGCTGAGGTTCTTTCGAGAATGGACGTCTCTGAGAGGCAA

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CAAGCTCGTCCTGCCATTCTTCTCTTCTCTCTCTCCAGTGCCTGGGCGGCAGAAGCCGGT
TGGGCCCTGATCCTTTTCAGGAACAAAGATCACTTCCAGTTACCAACCTCTTCGTGTGCG
GGCTACTGGCCAAAGCCCTACAGAACTCTTCGGCAGCTGGTGGCCAAAGGCTATCCTGA
GGAGGAAGCGCAAGGCCCTGTGGGCTCACCTGTTTGCTAGCCTGCGCTCCTACTTGAAGA
GCCTACCTCGGGTCCAGTCTGGAGGCTTTAACCAGGTGCATGCCATGCCACATTCTGT
GGATGCTGCGCTGCATCTATGAGACGCAGAGCCAGAAGGTGGGGCGCCTCGCCGCCAGGG
GCATCAGTGGGACTACCTCAAGCTGGCCTTTTGCAACGCTTGCTCTGCGGACTGCAGCG
CCCTGTCTCTCGTCTGCATCACTTCCACAGGCAGCTGGCCCTAGACCTGGACAACAACA
ACCTCAATGACTATGGCGTGCAGGAGCTGCAGCCTTGCTTTAGCCGTCTCACGGTTATCA
GACTCAGCGTCAACCAGATCACCGACACGGGGGTGAAGGTGCTATGTGAGGAACGACCA
AGTATAAGATCGTGACGTTCTCGGTTTATACAACAACCAGATAACTGATATCGGAGCCA
GGTATGTGGCCCAAATCTTGATGAATGCAGAGGCCCTCAAGCACCTTAACTAGGGAAAA
ACAGAATAACAAGTGAGGGCGGGAAGTGTGTGGCTTTGGCTGTGAAGAACAGCACCTCCA
TCGTTGATGTTGGGATGTGGGGTAATCAGATTGGAGACGAAGGGGCAAAGGCCTTCGCAG
AGGCATTGAAGGACCACCCCGCCTGACCACTCTCAGTCTTGCAATCAATGGCATCTCTC
CGGAGGGAGGGAAGAGCCTTGCGCAGGGCCCTGAAGCAGAACACCACACTGACAGTAATCT
GGCTGACCAAAAATGAACTTAATGATGAGTCTGCAGAGTGCTTCGCTGAGATGCTGAGAG
TGAACCAGACGCTACGGCATTTATGGCTGATCCAGAATCGCATCACAGCCAAGGGGACAG
CGCAGCTGGCGAGGGCACTGCAGAAGAACACAGCCATAACAGAGATTTGTCTCAATGGAA
ACTTGATTAAGCCCCAGGAGGCCAAAGTCTTCGAGAATGAGAAGAGAATCATCTGCTTCT
GACGGACGCTCCTGGGCAGGATCTTTGTCCTAGGTTGCTCCTCAGTCACAGACAGCACTG
TGCAGTCAGCAGGGTAGCAGGATGCTGTGCAGCGCCTGCAGCAAGGTGCCTGTGAGGAGC
CCACACCTCCACAGTGCACACCGATGTCCCTGCTCATGCTTGGACTGGTAGCACCCGCG
CCGCGGCTGAGACCCTGCAGACGCAGGGAGTCTTAGGAACCATCGTCACTCAAGGCC
AGCAGGGCATCTTCTGTACAAAGATCTCCCTGCATATCCACTAGACGGAAGCTGAAGGAA
CGCAACAGCAGAGGAGGCCAACAGACGCCTGGCTGAAGGCTCCGTGGGACCAACGGTGTG
ACCTTCAGAAAAGAGCTGGGAACCTTGAGCAGAGCCGATGGTAACCTTCTGGGGAAAGAAG
GCACCCAGTGACTGCATGGTTATTCTGAGTCTCTCTCTCTGCTTAGTCCCTCTCACTG
TACAGGTCTGTTTCTTCTCTCGCAGCTGTGGCTGCTGAAGTAGGTCCACTGTGGGGAGAGC
TCATCACAGACTTTGGTTTCGGTTCTGGATTCTCAGTGGTGGCAACCGAGAGTCAGACGAT
ACCCTCTAGGTGAGTCTCAGAGGATCTCTATGCTGTGAGAGGGTTGAGGGCCCCACCCAGA
ATTTTTTTTTTTTACCAGTTTTTACTGTGCCTGCCCCAGGAGGGAGAATTACTTCCCAGC

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CTCCACAGCAGCAGGCATGGCTTGCCTCAATGGTCCTCAGATCCCAACAAACTCTCTCC
CTTGCCTGTGAGCAGAAAGTATCTTCATGTCTCAGAAGTTGGAGGGTGACTGGACACAG
TTAAGACTCAGAGAGCCAGCTCATAAGCTCAAAGCAAAGCATGGCACATACCCACCACCAT
ACCATGGTGCGCATGGGATGGGACASTTGGAAATGTTGCAGATAACGTGTTCTTTTGGCCAG
TTCATTTGTTAATAAAATATTTAAAACGTTAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCG
G (SEQ ID NO:42)

FIG. 13 (Page 3 of 3)

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MEENGHHEMEGTPLGCHSHIKLLKINREHLVTNIRNTQCLVDNLLNGYFSAEDAEIVCA
OPTKPKVRKILDLVQSKGEEVSEFFLYVLQOLEDAYVDLRLNLSEIGFSPSQLIRTKTI
VNTDPVSRYTQQLRHQLGRDSKFMLCYAQKEDLLLEETYMDTLMGLVGFNNENLGSLGGL
DCLLDHSTGVLNEHGETVVFVG DAGVGKSMMLLQRLQSLWASGRLTSTAKFFFHFRCRMFS
CFKESDMLSLQDLLFKHFCYPEQDPPEEVFSFLLRFPHTALFTFDGLDELHSDFDLSRVPD
SCCFWEPAPHLVLLANLLSGRLLKGAGKLLTARTGVEVPRQLLRKKVLLRGFSPSHLRAY
ARRMFPERTAQEHLLOQLDANPNLCSLCGVPLFCWIIIFRCFQHFQTVFEGSSSQLPDCAV
TLTDVFLLVTEVHLNRPQPSLVQRNTRSPAETLRAGWRTLHALGEVAHRGTDKSLFVFG
QEEVQASKLQEGDLQLGFLRALPDVGPEQGQSYEFFHLLTQAFFTAFFLVADDKVSTREL
LRFFREWTSPGEATSSSSCHSSFFSFQCLGGRSRLGPDPPFRNKDHFQFTNLFVCGLLAKAR
QKLLRQLVPKAILRRKRKALWAHLFASLSYLKSLPRVQSGGFNQVHAMPTFLWMLRCIY
ETQSQKVGRILAARGISADYLKLAFCNACSDCSALSFVLHHFHRQLALDLDNNNLNDYGV
QELQPCFSRLTVIRLSVNQITDTGVKVLCEELTKYKIVTFLGLYNNQITDIGARYVAQIL
DECRGLKHLKLGKNRITSEGGKCVALAVKNSTSIVDVG MWGNQIGDEGAKAF AEALKDHP
SLTTLSLAFNGISPEGGKSLAQALKQNTTTLTVIWLTKNELNDESAECFAEMLRVNQTLRH
LWLIQNRITAKGTAQLARALQKNTAITEICLNGNLIKPEEAKVFENEKRIICF
(SEQ ID NO:43)

FIG. 16

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10	20	30	40	50	60	70	80	90
100	110	120	130	140	150	160	170	180
190	200	210	220	230	240	250	260	270
280	290	300	310	320	330	340	350	360
370	380	390	400	410	420	430	440	450
460	470	480	490	500	510	520	530	540
550	560	570	580	590	600	610	620	630
640	650	660	670	680	690	700	710	720
730	740	750	760	770	780	790	800	810
820	830	840	850	860	870	880	890	900
910	920	930	940	950	960			

MEHQHSEMGKFLGSHSHIOLKXNRELLMTRNTOCVLENLLNGVFSAEAEIVCACPTKPKVRKILLLVQSKGEEVSEFFLYVL 90
MEHQHSEMGKFLGSHSHIOLKXNRELLMTRNTOCVLENLLNGVFSAEAEIVCACPTKPKVRKILLLVQSKGEEVSEFFLYVL 90
MEHQHSEMGKFLGSHSHIOLKXNRELLMTRNTOCVLENLLNGVFSAEAEIVCACPTKPKVRKILLLVQSKGEEVSEFFLYVL 90

COLADAYVDRLWLEKGFSPSLASRVVAMPFVSEVTCOLGRDSCVFLCAQKEDLLLEETVADTINELVGFVSNESLGSLSGL 180
COLADAYVDRLWLEKGFSPSLASRVVAMPFVSEVTCOLGRDSCVFLCAQKEDLLLEETVADTINELVGFVSNESLGSLSGL 180
COLADAYVDRLWLEKGFSPSLASRVVAMPFVSEVTCOLGRDSCVFLCAQKEDLLLEETVADTINELVGFVSNESLGSLSGL 180

ACLLDHTSTGVINEOGETTFTLGDAGVCKSMILCQLQSLWASGRILTAKGFFFTHTCTVSCFESDRILSLODILFFHFCYPOODPEEVA 270
ACLLDHTSTGVINEOGETTFTLGDAGVCKSMILCQLQSLWASGRILTAKGFFFTHTCTVSCFESDRILSLODILFFHFCYPOODPEEVA 270
ACLLDHTSTGVINEOGETTFTLGDAGVCKSMILCQLQSLWASGRILTAKGFFFTHTCTVSCFESDRILSLODILFFHFCYPOODPEEVA 270

FLRFPFHVALFTFDGLDELHSDLSRVDPSSCFWEPAPHLVLLANLLSGRLLKAGKLLTARTGVEVFPOLLKXVLLRGFSPSHRAY 360
FLRFPFHVALFTFDGLDELHSDLSRVDPSSCFWEPAPHLVLLANLLSGRLLKAGKLLTARTGVEVFPOLLKXVLLRGFSPSHRAY 360
FLRFPFHVALFTFDGLDELHSDLSRVDPSSCFWEPAPHLVLLANLLSGRLLKAGKLLTARTGVEVFPOLLKXVLLRGFSPSHRAY 360

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ARRMFPERAAQDHLISOLDANPNLCSCVPLFCMIIFRCFQHFRAAFEGSSOLPDCAVILTDFVLLVTEVHLNMQPSSLVQNRTRSP 450
ARRMFPERAAQDHLISOLDANPNLCSCVPLFCMIIFRCFQHFRAAFEGSSOLPDCAVILTDFVLLVTEVHLNMQPSSLVQNRTRSP 450

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AEVTHAGRDITLHALGEVAHRGTKSLFVFCQEEVQASGLQEGDLOLGLRALPDVGRGGQOSYEFFHILTCAFFTAFFLVADDKVSTRE 539
AEVTHAGRDITLHALGEVAHRGTKSLFVFCQEEVQASGLQEGDLOLGLRALPDVGRGGQOSYEFFHILTCAFFTAFFLVADDKVSTRE 539

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VOELQPCFSLTVLRLSVNQITDGGVVLSEELTKIKIVTFLGLVANNQITDVGARYVAQILDECRGLKHL 809

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LAEMLKVNQTLKHLWLICNITAKGTAOLADALQNTGITEICLGNLILKPEAKVFEDEKRIICF 953

FIGURE 17

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FIG. 18 (1 of 10)

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tttgaggtgtgggggagaggtccaagtgaggatgccaagcagggttaactgcctccacgggacataca
aacaaggccgtggcattgatgagatcgggtggggaaaagggttagcccccacactggaggaaat
ctcagatgtagaggtcacatggaggagaatataggaaaggaaattgaagttagagtgctcagatgc
aggagaaaaatcagcgcatataaccaagccaaggggagggtgcctcaagaaggaggggagagga
gaggtcaggacagccaaaatcctgaggggccaagaaagacaagacctggaaaaatgtcattaaattc
aggcttatggagggtacaggtgacctagtgcagaccagtggaagagggatgggcagctggagag
gatccatgctaataatgaaggaactatctgcaaagggtatgttccttaatttcaggggatcatgtg

FIG. 18 (9 of 10)

[illegible]

1. *Chlorophyll a* (Chl *a*)
 2. *Chlorophyll b* (Chl *b*)
 3. *Chlorophyll c* (Chl *c*)
 4. *Chlorophyll d* (Chl *d*)
 5. *Chlorophyll e* (Chl *e*)
 6. *Chlorophyll f* (Chl *f*)
 7. *Chlorophyll g* (Chl *g*)
 8. *Chlorophyll h* (Chl *h*)
 9. *Chlorophyll i* (Chl *i*)
 10. *Chlorophyll j* (Chl *j*)
 11. *Chlorophyll k* (Chl *k*)
 12. *Chlorophyll l* (Chl *l*)
 13. *Chlorophyll m* (Chl *m*)
 14. *Chlorophyll n* (Chl *n*)
 15. *Chlorophyll o* (Chl *o*)
 16. *Chlorophyll p* (Chl *p*)
 17. *Chlorophyll q* (Chl *q*)
 18. *Chlorophyll r* (Chl *r*)
 19. *Chlorophyll s* (Chl *s*)
 20. *Chlorophyll t* (Chl *t*)
 21. *Chlorophyll u* (Chl *u*)
 22. *Chlorophyll v* (Chl *v*)
 23. *Chlorophyll w* (Chl *w*)
 24. *Chlorophyll x* (Chl *x*)
 25. *Chlorophyll y* (Chl *y*)
 26. *Chlorophyll z* (Chl *z*)
 27. *Chlorophyll aa* (Chl *aa*)
 28. *Chlorophyll ab* (Chl *ab*)
 29. *Chlorophyll ac* (Chl *ac*)
 30. *Chlorophyll ad* (Chl *ad*)
 31. *Chlorophyll ae* (Chl *ae*)
 32. *Chlorophyll af* (Chl *af*)
 33. *Chlorophyll ag* (Chl *ag*)
 34. *Chlorophyll ah* (Chl *ah*)
 35. *Chlorophyll ai* (Chl *ai*)
 36. *Chlorophyll aj* (Chl *aj*)
 37. *Chlorophyll ak* (Chl *ak*)
 38. *Chlorophyll al* (Chl *al*)
 39. *Chlorophyll am* (Chl *am*)
 40. *Chlorophyll an* (Chl *an*)
 41. *Chlorophyll ao* (Chl *ao*)
 42. *Chlorophyll ap* (Chl *ap*)
 43. *Chlorophyll aq* (Chl *aq*)
 44. *Chlorophyll ar* (Chl *ar*)
 45. *Chlorophyll as* (Chl *as*)
 46. *Chlorophyll at* (Chl *at*)
 47. *Chlorophyll au* (Chl *au*)
 48. *Chlorophyll av* (Chl *av*)
 49. *Chlorophyll aw* (Chl *aw*)
 50. *Chlorophyll ax* (Chl *ax*)
 51. *Chlorophyll ay* (Chl *ay*)
 52. *Chlorophyll az* (Chl *az*)
 53. *Chlorophyll ba* (Chl *ba*)
 54. *Chlorophyll bb* (Chl *bb*)
 55. *Chlorophyll bc* (Chl *bc*)
 56. *Chlorophyll bd* (Chl *bd*)
 57. *Chlorophyll be* (Chl *be*)
 58. *Chlorophyll bf* (Chl *bf*)
 59. *Chlorophyll bg* (Chl *bg*)
 60. *Chlorophyll bh* (Chl *bh*)
 61. *Chlorophyll bi* (Chl *bi*)
 62. *Chlorophyll bj* (Chl *bj*)
 63. *Chlorophyll bk* (Chl *bk*)
 64. *Chlorophyll bl* (Chl *bl*)
 65. *Chlorophyll bm* (Chl *bm*)
 66. *Chlorophyll bn* (Chl *bn*)
 67. *Chlorophyll bo* (Chl *bo*)
 68. *Chlorophyll bp* (Chl *bp*)
 69. *Chlorophyll bq* (Chl *bq*)
 70. *Chlorophyll br* (Chl *br*)
 71. *Chlorophyll bs* (Chl *bs*)
 72. *Chlorophyll bt* (Chl *bt*)
 73. *Chlorophyll bu* (Chl *bu*)
 74. *Chlorophyll bv* (Chl *bv*)
 75. *Chlorophyll bw* (Chl *bw*)
 76. *Chlorophyll bx* (Chl *bx*)
 77. *Chlorophyll by* (Chl *by*)
 78. *Chlorophyll bz* (Chl *bz*)
 79. *Chlorophyll ca* (Chl *ca*)
 80. *Chlorophyll cb* (Chl *cb*)
 81. *Chlorophyll cc* (Chl *cc*)
 82. *Chlorophyll cd* (Chl *cd*)
 83. *Chlorophyll ce* (Chl *ce*)
 84. *Chlorophyll cf* (Chl *cf*)
 85. *Chlorophyll cg* (Chl *cg*)
 86. *Chlorophyll ch* (Chl *ch*)
 87. *Chlorophyll ci* (Chl *ci*)
 88. *Chlorophyll cj* (Chl *cj*)
 89. *Chlorophyll ck* (Chl *ck*)
 90. *Chlorophyll cl* (Chl *cl*)
 91. *Chlorophyll cm* (Chl *cm*)
 92. *Chlorophyll cn* (Chl *cn*)
 93. *Chlorophyll co* (Chl *co*)
 94. *Chlorophyll cp* (Chl *cp*)
 95. *Chlorophyll cq* (Chl *cq*)
 96. *Chlorophyll cr* (Chl *cr*)
 97. *Chlorophyll cs* (Chl *cs*)
 98. *Chlorophyll ct* (Chl *ct*)
 99. *Chlorophyll cu* (Chl *cu*)
 100. *Chlorophyll cv* (Chl *cv*)
 101. *Chlorophyll cw* (Chl *cw*)
 102. *Chlorophyll cx* (Chl *cx*)
 103. *Chlorophyll cy* (Chl *cy*)
 104. *Chlorophyll cz* (Chl *cz*)
 105. *Chlorophyll da* (Chl *da*)
 106. *Chlorophyll db* (Chl *db*)
 107. *Chlorophyll dc* (Chl *dc*)
 108. *Chlorophyll dd* (Chl *dd*)
 109. *Chlorophyll de* (Chl *de*)
 110. *Chlorophyll df* (Chl *df*)
 111. *Chlorophyll dg* (Chl *dg*)
 112. *Chlorophyll dh* (Chl *dh*)
 113. *Chlorophyll di* (Chl *di*)
 114. *Chlorophyll dj* (Chl *dj*)
 115. *Chlorophyll dk* (Chl *dk*)
 116. *Chlorophyll dl* (Chl *dl*)
 117. *Chlorophyll dm* (Chl *dm*)
 118. *Chlorophyll dn* (Chl *dn*)
 119. *Chlorophyll do* (Chl *do*)
 120. *Chlorophyll dp* (Chl *dp*)
 121. *Chlorophyll dq* (Chl *dq*)
 122. *Chlorophyll dr* (Chl *dr*)
 123. *Chlorophyll ds* (Chl *ds*)
 124. *Chlorophyll dt* (Chl *dt*)
 125. *Chlorophyll du* (Chl *du*)
 126. *Chlorophyll dv* (Chl *dv*)
 127. *Chlorophyll dw* (Chl *dw*)
 128. *Chlorophyll dx* (Chl *dx*)
 129. *Chlorophyll dy* (Chl *dy*)
 130. *Chlorophyll dz* (Chl *dz*)
 131. *Chlorophyll ea* (Chl *ea*)
 132. *Chlorophyll eb* (Chl *eb*)
 133. *Chlorophyll ec* (Chl *ec*)
 134. *Chlorophyll ed* (Chl *ed*)
 135. *Chlorophyll ee* (Chl *ee*)
 136. *Chlorophyll ef* (Chl *ef*)
 1

FIG. 19

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0072971.1000

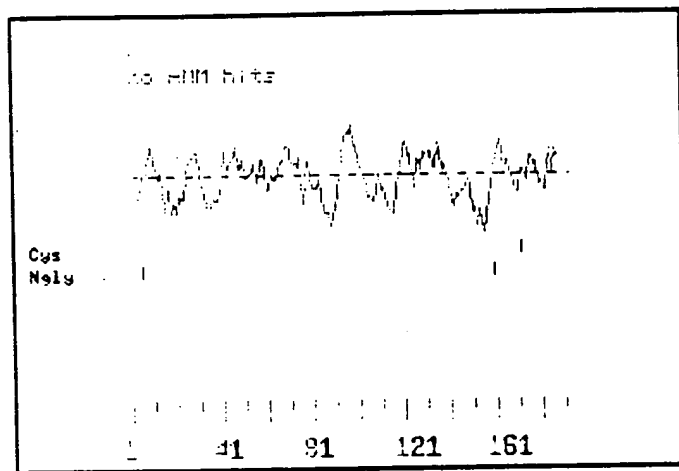


FIG 20

[illegible]

721 A.TACGAAAAGCCAGCTTGAA
TATGCTTTTCGGTCGAACTT

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00T03E " T202450

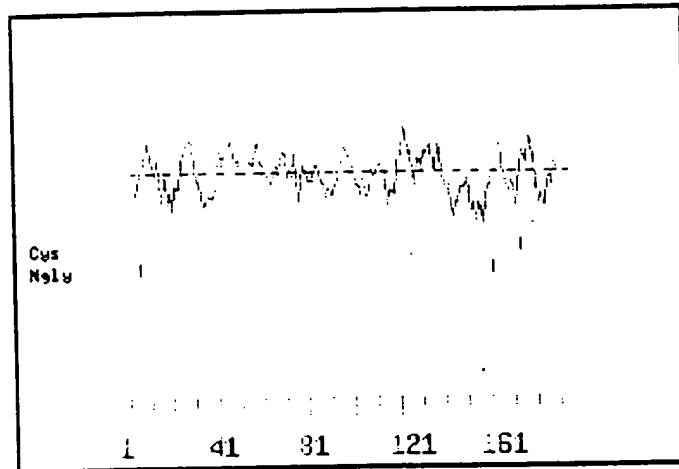


FIG. 22

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ALIGN calculates a global alignment of two sequences
version 2.0>Please cite: Myers and Miller, CABIOS (1989)
> hCARD5-DNA                                740 aa vs.
> mCARD5-DNA                                763 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
68.2% identity;    Global alignment score: 2377

      10      20      30
inputs C---GCGTCCGGCTGCAG-CGGGGTG-----AGCG-GCGGCAGC-----GGC
      :  :::::::::::::::  ::  ::  :::::::::::::::  ::
      CCACGCGTCCGGCAGCAGGCTGCAGCAGGCGAGCAGCAGCAAGAGTAAAAGGTGAC
      10      20      30      40      50      60

      40      50      60      70      80      90
inputs CGGGGAT-----CCTGGAGCCATGGGGCGCGCGCGCAGCCATCCTGGATGCGCTGGA
      :  ::  :  ::  :::::::::::::::  ::  ::  :::::::::::::::  ::  ::
      CGCGGCTGCCCCACCCAGAGCCATGGGGCGGGCAGAGATGCCATCCTGGACGCTCTTGA
      70      80      90      100     110     120

      100     110     120     130     140     150
inputs GAACCTGACCGCCGAGGCTCAAGAAGTTCAAGCTGAAGCTGCTGTCGGTGCCGCTGCG
      :  ::  :  :  ::  :::::::::::::::  ::  ::  :::::::::::::::  ::  ::
      AAACCTGTGTCAGGGGATGAACCTCAAAAAGTTCAAGATGAAGCTGCTGACAGTGCAACTGCG
      130     140     150     160     170     180

      160     170     180     190     200     210
inputs CGAGGGCTACGGGCGCATCCCGCGGGGCGCGCTGCTGTCCATGGACGCCTTGACCTCAC
      :  ::  ::  :::::::::::::::  :  :  :::::::::::::::  :::::::::::::::
      AGAAGGCTATGGGCGCATCCACGCGGGGCCCTGCTGCAGATGGACGCCATAGATCTCAC
      190     200     210     220     230     240

      220     230     240     250     260     270
inputs CGACAAGCTGGTCAGCTTCTACCTGGAGACCTACGGCGCCGAGCTACCCGCTAAC-GTGC
      :  ::  ::  :::::::::::::::  :  :  :::::::::::::::  :::::::::::::::
      TGACAAACTTGTGCTAGCTACTATCTGGAGTCGTATGGCTTGGAGCTCAC-AATGACTGTGC
      250     260     270     280     290

      280     290     300     310     320     330
inputs TGCGCGACATGGGCCTGCAGGAGATGGCCGGGCAGCTGCAGGCGGCCACGCACCAGGGCT
      :  :  :::::::::::::::  :::::::::::::::  :::::::::::::::  :  :  ::
      TTAGAGACATGGGCTTACAGGAGCTGGCTGAGCAGCTGCAAACGACTAAAGA--AGAG-T
      300     310     320     330     340     350

      340     350     360     370     380     390
inputs CTGGAGCCGCGCCAGCTGGGATCCAGGCCCTCCTCAGTCGGCAGCCAAAGCCAGGCCTGC
      :  ::  :  :  ::  ::  :  :  :  :  ::  ::  :  :  :  :  ::  ::  :  :
      CTGGAGCTGTGGCAGCTGCAGCCAGTGTCCCTGCTCAGAGTACAGCCAGAACAGG---AC
      360     370     380     390     400     410

      400     410     420     430     440     450

```

FIG. 23 (1 of 2)

FIG 23 (2 of 2)

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ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
 > hCARD5-protein 195 aa vs.
 > mCARD5-protein 193 aa
 scoring matrix: paml20.mat, gap penalties: -12/-4
 71.8% identity; Global alignment score: 712

```

      10      20      30      40      50      60
inputs MGRARDAILDALENLTAEELKKFKLKLLSVPLREGYGRIPRGALLSMDALDLTDKLVSYF
      .....
      MGRARDAILDALENLSGDELKKFKMKLLTVOLREGYGRIPRGALLQMDAIDLTDKLVSYF
      10      20      30      40      50      60

      70      80      90     100     110     120
inputs LETYGAELTANVLRDMGLQEMAGQLQAATHQGSGAAPAGIQAPPQSAAKPGLHFIDQHRA
      .....
      LESYGLELTMTVLRDMGLQELAEQLQT-TKEESGAVAAAASVPAQSTARTG-HFVDQHRQ
      70      80      90     100     110

      130     140     150     160     170     180
inputs ALIARVTNVEWLLDALYGKVLTDQYQAVRAEPTNPSKMRKLFSFTPAWNWTCKDLLLQA
      .....
      ALIARVTEVDGVLDALHGSVLTEGQYQAVRAETTSQDKMRKLFSFVPSWNLTKDSSLQA
      120     130     140     150     160     170

      190
inputs LRESQSYLVEDLERS
      .....
      LKEIHPYLVMDLEQS
      180     190

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1 CCCGCGTCCGGACTTCCCTTCCAGTGTTCCTCTCTGCTCTCTCCAACAGAAGGTATTTTIG
GGGCGCAGGCCTGAAGGGAAGGTACAAACAAGGAGACGAGAGAGGTTGTCTTCCATAAAAAC

66 GCATGTTTTATCTTTGCTAAGTAGGATTTCTGTCTTTCTTTGTTAACACAGATTTCTTTCTGTGC
CGTACAAAATAGAAACGATTTCCTTAAAGACAGAAAGAAACAATTGTGTCTAAAGAAAGACAG

131 CAGAATGACCTGATCCATTTCTGGTTTGTAGAAAGCCATGGCTTCAGAGGGTGCTTCTCTCAGAA
GTCTTACTGGACTAGGTAAAGGACCAACATCTTTCCGGTACCGAAGTCTCCCACGAAGGAGTCTT
----- 1 M A S E G A S S E -----

196 ATCATAGAAAAACAGCGAACAAAGTTGCTCAGTGTCTTCCAACAAGATCCCGACTCTATCTTGA
TAGTATCTTTTGTGCTTGTTCACGAGTCAACAGGAGGTGTTCTAGGGCTGAGATAGAACCT
----- 10 I I E K Q R T K L L S V L Q Q D P D S I L D -----

261 CACGTTAACCTCTCGGAGACTGATTTCTGAGGAGGAGTATGAGACTCTAGAGGCAATTACAGATC
GTGCAATTGGAGAGCCTCTGACTAAAGACTCTCTCCTCATACTCTGAGATCTCCGTTAATGTCTAG
----- 31 T L T S R R L I S E E Y E T L E A I T D -----

326 CTCTGAAGAAAAGCCGAAGCTGTTAATTTTGATCCAGAAGAAGGGAGAGGACAGCTGTTGTGT
GAGACTTCTTTTCGGCCTTCGACAATTAAACTAGGTCTTCTTCCCTCTCTGTGCGACAACAACA
----- 53 P L K K S R K L L I L I Q K K G E D S C C C -----

391 TTCCTCAAGTGTCTGTCTAATGCCTTTCCACAGTCAGCTTCCACCTTGGGTTTAAAGCAGGAAGT
AAGGAGTTCACAGACAGATTACGGAAGGTGTGAGTCAAGGTGGAACCCAAATTTCTGCTCTCA
----- 75 F L K C L S N A F P Q S A S T L G L K Q E V -----

456 TCCACGGCAGGGGACTGGAGAGGTTGTGAGGTGAGCAGGGGTTTGAAGATCCCTTTTCTCTTG
AGGTGCCGTCCCCTGACCTCTCCAACAGCTCCACTCGTCCCCAAACCTTCTAGGGAAAAGAGAAC
----- 96 P R Q G T G E V V E V S R G L E D P F S L -----

521 GGACCATAACCCAGAAATAGCAGAGCTCTCAGAAGAGAAAGAATGCCCGGGTCTGGGAGCTCCG
CCTGGTATTTGGGGTCTTTATCGTCTCGAGAGTCTTCTTTCTTACGGGCCAGACCCTCGAGGC
----- 118 G T I T P E I A E L S E E K E C P G L G A P -----

586 GAGTTCTTCACCTGCAAGGAAAGCAGCCACAGGGAACCGGAAGTACCTTCTTGGGAGAATCAGGA
CTCAAGAAAGTGACGTTCCCTTTCGTGCGTGTCCCTTGGCCTTCATGGAAGAACCCTCTTAGTCCT
----- 140 E F F T C K E S S H R E P E V P S W E N Q E -----

651 AGGGCGTGGTGCACAGCAAGTCACCGCTCCGCGTTCAGTCAAAGGAGTTGAGTATGAAGTTCCAG
TCCCGCACCACTGTCGTTTCAGTGGCGAGGCGCAAGTCAGTTTCTCAACTCATACTTCAAGGTC
----- 161 G R G A Q Q V T A P R S V K G V E Y E V P -----

[illegible]FIG. 25 (20×7)

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1431 ACAGTCCTCAGGAGGGCCCCCTCAGGGAAACAGACACATTTCTGGGTCTCACAAGATGCCTGTCA
TGTGAGGAGTCCTCCCGGGAGTCCCTTTGTCTGTGTAAAGACCCAGAGTGTCTTACGGACAGT
421▶ Q S S G G P L R E T D T F L G L T K M P V

1496 TCTCTTTTGTGCGACTAGGACGCTGCAGCTTCTCCAAGTCCAGAATTGTAAACACACTGCTCAGC
AGAGAAAACACGCTGATCCTGCGACGTCGAAGAGGTTAGGTCTTAACAATTGTGTGACGAGTCG
443▶ I S F V R L G R C S F S K S R I V N T L L S

1561 TCCTCCCAGCAGAAACCATACCCGATTTTCTCCATCAGGATCTGTCTGTCCCTGTGCTTCTCTCG
AGGAGGGTCTCTTTGGTATGGGCTAAAAGGAGGTAGTCCTAGACAGACAGGGACACGAAGGAGC
465▶ S S Q Q K P Y P I F L H Q D L S V P V L P R

1626 GCAAAATTTCTGACGGCCTGGTGGAAAGTGACATGGTGCTTTCTGACAAGTTGCTGAAGGAAAGCC
CGTTTAAAGACTGCCGACCACCTTCACTGTACCACGAAAGGACTGTTCAACGACTTCTTTTCGG
486▶ Q I S D G L V E V T W C F P D K L L K E S

1691 CGCATGCTTTCCAGAAACCTGTTGCTGTGGCCAACCTTCGTGGAGATTTAGAAAGCTTTTGGATA
GCGTACGAAAGGTCTTTGGACAACGACACCGGTTGGAAGCACCTCTAAATCTTTTCGAAAACCTAT
508▶ P H A F Q K P V A V A N L R G D L E S F W I

1756 CAATTTGGTTTCTGCTAGAAAGTTTCTCCGGTCTTTCTTTTTCACAGACTGCCTTGGTGAGAA
GTTAAACCAAAGGACCATCTTCAAAGGAGGCCAGAAAAGAAAAGTGTCTGACGGAACCACTCTT
530▶ Q F G F L V E V S S G L F F F T D C L G E K

1821 GGAATGGGACTTGTCTAATGTTTATAGGAGAGGACACCATTGAACGGTGCTACTTTATCCTCAGTC
CCTTACCCTGAACGATTACAAAATCTCTCTCTGTGGTAACTTGCCACGATGAAATAGGAGTCAG
551▶ E W D L L M F L G E D T I E R C Y F I L S

1886 CCCAGGCTAAGGAGAGTGAAGAAGCCCAGATTTTCCAAGGATCCTAAAACCTGAAGCEATCTCAG
GGGTCCGATTCCTCTCACTTCTTCGGGTCTAAAAGGTTTCTTAGGATTTTGAAGTCCGGTAGAGTC
573▶ P Q A K E S E E A Q I F Q R I L K L K P S Q

1951 CTACTGTTTGGGAAGCTGAGGAAGCTGGGGATAGAAGGAAGACTATGGAGGCCCTTCAAGCTGC
GATGACAAAACCTTCGACTCCTTCGACCCCTATCTTCTCTGATACCTCCGGAAGTTTCGACG
595▶ L L F W E A E E A G D R R K T M E A L Q A A

2016 CCTCCAGGAAGTAATGTCCTCTCCACTCAGATGTGTGTCCTTGAAGAGATGGCCTCTCTGGCCA
GGAGGTCTTCAATTACAGGAGAGGTGAGTCTACACACAGGGAACCTTCTTACCGGAGAGACCGGT
616▶ L Q E V M S S P L R C V S L E E M A S L A

2081 GGGAGCTGGGCATTTCAGGTAGACCAAGACTTTGAAGTTACTCAAGATATTCAAGTTTCCCCCACA
CCCTCGACCCGTAAGTCCATCTGGTCTGAAACTTCAATGAGTTCTATAAGTTCAAAGGGGGTGT
638▶ R E L G I Q V D Q D F E V T Q D I Q V S P T

2796 GCCTTCTCAGCAGAGACCCAGTCAGCCTAAATCATTCCAGACCAAGCCTTCACAGGCCAGGGCCT
CGGAAGAGTCGTCCTCTGGGTCAgTCGGATTTAGTAAGGTCGGTTCGGAAGTGTCGGTCCCGGA
876▶ P S Q Q R P S Q P K S F Q T K P S Q A R A

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2861 GCCACCCAAGAGCAGGGAGACGTTAAAGAACATACTCTGGAGATCTGGGAAATAAAGTATGGGCT
CGGTGGGTTCCTCGTCCCTCTGCAATTTCTTGATGAGACCTCTAGACCCCTTTATTTTCATACCCGA
898 C H P R A G R R

2926 TTGCTTAAGTATTCTTTTTCATATAGCAAGCTGAAGAAAAGTTTTAGTGAAAGACTGATAAAAAGT
AACGAATTCATAAGAAAAAGTATATCGTTCGACTTCTTTTCAAAATCACTTTCTGACTATTTTCA

2991 AGCAAAACCCAAAAAGGTATGCAAAGTCTTAAGTGCATAGCAAAGTATCCAAGTGTGGGAAATA
TCGTTTTGGGTTTTTTCCATACGTTTCAGAAATTCACGTATCGTTTTCATAGGTTACACCCCTTTAT

3056 TGGAAAGCAGTTAAAAGTAGAATCTGGCTGGGCA TGGTGGCACACATCTACAGGTTTTAGCATGGG
ACCTTCGTCAATTTTCATCTTAGACCCGACCCGTACCACCGTGTGTAGATGTCCCAAATCGTACCC

3121 AGGGCTCTGTCTATCCCACTCAGAGAAGCAGGCAGATCTCTGTGTGTTTTGAGGCCAGTCTGGTCT
TCCCGAGACAGTAGGGTTGAGTCTCTTCGTCCGTCTAGAGACACACAAACTCCGGTCAGACCCAGA

3186 ACATAACAACGACACAAGCAAGTCCCTACATCAGCCATACTACAAAATGAGACCCCATCTGGGGAC
TGTATTGTTGCTGTGTTTCGTTTCAGGATGTAGTCGGTATGATGTTTTACTCTGGGGTAGACCCCTG

3251 AAAAGGGTTGGATCTAACATCAAACCAAAGAAATCAGTCAAGTATTCCAGAAGGCATCATTAAAT
TTTTCCCAACCTAGATTGTAGTTTGGTTTTCTTTAGTCAGTTCATAAGGTCTTCGGTAGTAATTAA

3316 ACACTCAGTGGGTTACCACAACCAAACCATACTCGACAACCTAACCCCTTAAAGGAGCAAGAAGGA
TGTGAGTCACCCAATGGTGTGGTTTCGTATGAGCTGTTGATTGGGGGATTTCTCTCGTTCTTCCT

3381 GTTGGGTGGGTGTTAGGCTGAACATGATTGGGGAAGAACTGAAGATAGATAAGGTCATTTCGTAAT
CAACCCACCCACAATCCGACTTGTACTAACCCCTTCTTGACTTCTATCTATTCCAGTAAGCATTAA

3446 ACAGGTTATGGGACTTGTCAAATCCATTAAATGCAATATTAAGAAGCAGTGGGAATCTTAAGGCT
TGTCCAATACCCCTGAACAGTTTAGGTAATTTACGTTATAATTTCTTCGTACCCCTTAGAATTCGGA

3511 ACATTAAAGCTCCAGTGAGTCGCAACCCCTCCCTTATTAGATGATGTGAGATTTGAACCCCACTGAA
TGTAATTCGAGGTCACTCAGCGTTGGGAGGGGATAATCTACTACACTCTAAACTTGGGGTCACTT

3576 TGGGGTGTGTCTGATAGCCCGTGTGTGTGACAACTGTGTAATTATAAAGTGATGAAAACGTGGG
ACCCACACAGACTATCGGGCACACACTGTTTGACACATTAATATTTCACTACTTTTGCACCC

3641 AGTTCAGCTTATCTGTGTTGAAGAAAGGCTGCTTCAGAGGTGCCTTGGTTTTGGGTTTATGATCA
TCAAGTCGAATAGACACAACCTCTTTCCGACGAAGTCTCCACGGAACCAAAACCAAACTACTAGT

007207.42260

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3706 GCCACTGAGCAGATACTCTGCACCAATTGGTACAGTTAAATCAGCTTGCTTCTGGTAATAGCCCCA
CGGTGACTCGTCTATGAGACGTGGTAACCAATGTCAATTTAGTCCAACGAAGACCATTATCGGGGT

3771 ATCTACCACATTTATCCCTTACAGGCGGAAATAATGAATGATCAGCAAAACATCCAATTTTACCT
TAGATGGTGTAAATAGGGAATGTCCGCCCTTATTACTTACTAGTCGTTTGTAGGTTAAATGGA

3836 TAACCTTGGTACTGATTGTATATGTATCATTTCTTATATAATAGCTAAGAAAATTTAGCTCATT
ATTGGAACCATGACTAAACATATACATAGTAAGAAATATATTATCGATTCCTTTTAAATCGAGTAA

3901 AGGGGTTCCTGATATATTAGTTTAAATGGTTTGAAGTCAGAAATGTGTTAGTTTAAATTTTAGAGT
TCCCCAAGACTATATAATCAAATTACCAAACCTTCAGTCTTTACACAATCAAAAATTTAAATCTCA

3966 TAATTGAAAATATTGAGATGAATTTACAAAGGCTATAAGTAATGTTTGTAGAGGGTTATAATTTT
ATTAACTTTTATAACTCTACTTAAATGTTTCCGATATTCATTACAAACTCTCCCATATTAAAAA

4031 GTAGACTCATACTGTTCTGAACATTTGGATAGCTTCTCGTAGTTAGCAGTGTTATAGAAGAATAT
CATCTGAGTATGACAAGACTTGTAAACCTATCGAAGAGCATCAATCGTCACAATATCTTCTTATA

4096 ATTTGATTTCAGGTATTTAACCAGAGCTGCTCTTAGTTTAAAGTGTACCAAGAGTCAATAAAAG
TAAACTAAGTCCATAAATTTGGTCTCGACGAGAATCAAAAATTCACAGTGGTTCTCAGTTATTTTC

4161 GCTACATTATCTGAACATGTGGGAACACAACCTGTGACCTTACACTTAAGAGACTGAGGAAGGGAA
CGATGTAATAGACTTGTACACCTTGTGTTGACACTGGAATGTGAATTCCTGACTCCTTCCCTT

4226 ATCAAGGTTCAAGCCAGCAGCACATAGTGAGACCAGGTCTCAAGACACAAAACTATCCACCTTA
TAGTTCCAAGTTCGGTCTGCTGTATCACTCTGGTCCAGAGTTCTGTGTTTTTGTATAGGTGGAAT

4291 AGGAAGATTTTAAATTTGCCTCATTAAGAAATAAGTAAGATTTATAAATTTGACTAAATGTCA
TCCCTCTAAAAATTTTAAACGGAGTAATTCCTTTATTTTCAATCTAAATATTTAACCTGATTACAGT

4356 CATCTTTGAACTTATGACTGTTTAAATTTTGTGACTTAAAGTTTAAATTTTATTATTGTATGCGTGT
GTAGAAACTTGAATACTGACAAATTTAAAAAACTGAATTTCAAATTTAAATAATAACATACGCACA

4421 GTTGTATGTGTGTCACATGTGTGCCACTGCATGTATGTGGAGGCCATCAGACAATGTTGTAGAG
CAACATACACACAGTGTACACACGGTGACGTACATACACCTCCGGTAGTCTGTTACAACATCTC

4486 TCTGTTCTTTCTCTTAGCCCTATGTGTTTTACCCACTGAGCTAGGCCACCTACTCCTATAAGTC
AGACAAGAAAGGAGAATCGGGATACACAAAATGGGTGACTCGATCCGGTGGATGAGGATATTTCAG

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4551 TAATTTTAAATAGTAAATAGTTCTAAGAAGTCAATCAGGGAAAAAATGGCTGTCAAAGTCTCA
ATTAAAAATTTATCATTTTATCAAGATTCTTCAGTTAGTCCCTTTTTTTACCGACAGTTTCAGAGT

4616 AAGAAAAATCGTATTAGCCATGGATAGAGACTCACCTCTTGAAATCATTTGTGTCTGAGAATAGCC
TTCTTTTTAGCATAATCGGTACCTATCTCTGAGTGGAGAAGTTAGTAAACACAGACTCTTATCGG

4681 TAATATCACAATAATGTGTTTGTACATGTGTTAGTTAATATTGTTTTTCAGAGTATTTAATCTCTC
ATTATAGTGTATTACACAAACATGTACACAAATCAATTATAACAAAAGTCTCATAAATTAGAGAG

4746 ATGATTATTGTAAAGATGAAAAAGAAATAGTGGGCAATGTATGTGAGTATTTAATTTTCCTGA
TACTAATAACATTTCTACTTTTTCTTTATCACCCGTTACATACACTCATAAATTAAACGGACT

4811 CAATTCCTGTCTTTTGAATGATAAATGTAAGAAGTAAAATAAAACGGTTTCATTTCTCAGAACAACT
GTTAAGACAGAAAAATCTTACTATTTACATTTCTCATTTTTATTTTGCCAAGTAAGAGTCTTGTGTA

4876 AAGCCAGCTCACTTAAGTCTGGGCCCTGCTGGCATTGGCTAGTCTAGCTACCCCCACCCAAACAC
TTCCGTCTGAGTGAATTCAGACCCGGGACGACCGTAACCGATCAGATCGATGGGGGTGGGTTTGTG

4941 AAAAGTTTAGAGAAGAAAAATGACTGAGTCAAGCTTGCCTAATGACTTTTGGACATAAAGTTTATG
TTTTCAAATCTCTTCTTTTACTGACTCAGTTTGAACGGATTACTGAAAACCTGTATTTCAAATAC

5006 GTCCTAGAAAGCCTTAAAAATAAGTAGGATATAAAACATGTAAATTAACCCACACATTATGTGGGT
CAGGATCTTTCCGAATTTTATTCATCCTATATTTGTACATTTAATTGGGTGTGTAATACACCCA

5071 TGAGAAGCAGAAAAATGTCAGTAGAACACTCGGCCAGTGCATAAAGAAGGAAGAGACCTCTGTTT
ACTCTTCGTCTTTTACAGTCACTCTGTGAGCCGGTCACGTATTTCTTCTCTCTGGAGACAAG

5136 TGGGTTATAAAACTGCTCTTTGTGCTCAATTTGTCCCTGCTTTTGTGTTGCCAGAATGTACAAGA
ACCCAATATTTTGACGAGAAACACGAGTTAAACAGGGGACGAAAACAAACGGTCTTACATGTTCT

5201 TTATAAAATAAACTCACTTTTACTTTTTAAAAAAGGGCGG
AATATTTTATTTGAGTGAAAAATGAAAAATTTTTTTTTTTTTTTTCCCGCC

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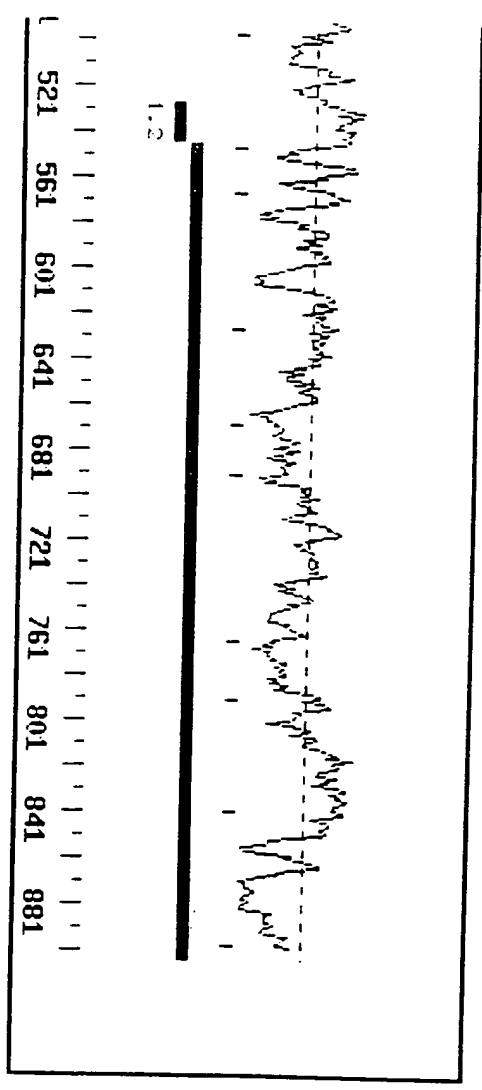
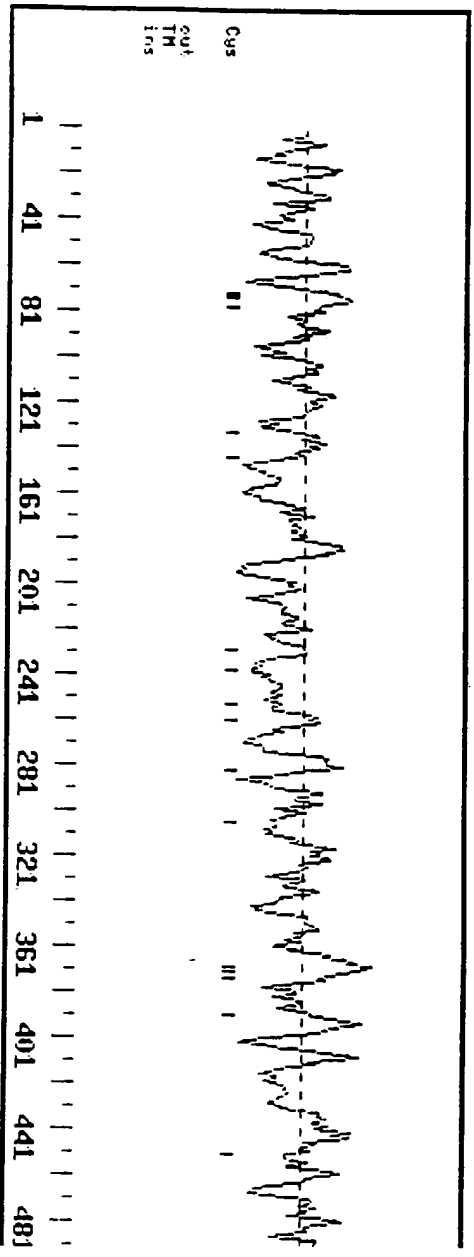


FIG. 26

09728721.120100

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100																																																																																																																																																											
0	00000000	00000001	00000010	00000011	00000100	00000101	00000110	00000111	00001000	00001001	00001010	00001011	00001100	00001101	00001110	00001111	00010000	00010001	00010010	00010011	00010100	00010101	00010110	00010111	00011000	00011001	00011010	00011011	00011100	00011101	00011110	00011111	00100000	00100001	00100010	00100011	00100100	00100101	00100110	00100111	00101000	00101001	00101010	00101011	00101100	00101101	00101110	00101111	00110000	00110001	00110010	00110011	00110100	00110101	00110110	00110111	00111000	00111001	00111010	00111011	00111100	00111101	00111110	00111111	01000000	01000001	01000010	01000011	01000100	01000101	01000110	01000111	01001000	01001001	01001010	01001011	01001100	01001101	01001110	01001111	01010000	01010001	01010010	01010011	01010100	01010101	01010110	01010111	01011000	01011001	01011010	01011011	01011100	01011101	01011110	01011111	01100000	01100001	01100010	01100011	01100100	01100101	01100110	01100111	01101000	01101001	01101010	01101011	01101100	01101101	01101110	01101111	01110000	01110001	01110010	01110011	01110100	01110101	01110110	01110111	01111000	01111001	01111010	01111011	01111100	01111101	01111110	01111111	10000000	10000001	10000010	10000011	10000100	10000101	10000110	10000111	10001000	10001001	10001010	10001011	10001100	10001101	10001110	10001111	10010000	10010001	10010010	10010011	10010100	10010101	10010110	10010111	10011000	10011001	10011010	10011011	10011100	10011101	10011110	10011111	10100000	10100001	10100010	10100011	10100100	10100101	10100110	10100111	10101000	10101001	10101010	10101011	10101100	10101101	10101110	10101111	10110000	10110001	10110010	10110011	10110100	10110101	10110110	10110111	10111000	10111001	10111010	10111011	10111100	10111101	10111110	10111111	11000000	11000001	11000010	11000011	11000100	11000101	11000110	11000111	11001000	11001001	11001010	11001011	11001100	11001101	11001110	11001111	11010000	11010001	11010010	11010011	11010100	11010101	11010110	11010111	11011000	11011001	11011010	11011011	11011100	11011101	11011110	11011111	11100000	11100001	11100010	11100011	11100100	11100101	11100110	11100111	11101000	11101001	11101010	11101011	11101100	11101101	11101110	11101111	11110000	11110001	11110010	11110011	11110100	11110101	11110110	11110111	11111000	11111001	11111010	11111011	11111100	11111101	11111110	11111111

FIG 27

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CACGCGTCCGCCGGATCAGAGAGTGCTCCGAGCTGGGTTGCCCCACTGTGCTTGTATCTGCACTCTCCAACACTAGGC 79
 ATCATTGACATGTTAAAGCTTAGCCAAATAGAATTGTTCTTTGTCACTCTTTTAACTTTTACTTATTCATTAGGAT 158
 GATTTTCATAATATATTTCTGTTTAGAGGAAACAGGAACA M A T E S T P S E 9
 ATG GCT ACC GAG AGT ACT CCC TCA GAG 226
 I I E R E R K K L L E I L Q H D P D S I 29
 ATC ATA GAA AGA GAA AGA AAA AAG TTG CTT GAA ATC CTT CAA CAT GAT CCT GAT TCT ATC 286
 L D T L T S R R L I S E E E Y E T L E N 49
 TTA GAC ACG TTA ACT TCT CGG AGG CTG ATT TCT GAG GAA GAG TAT GAG ACT CTG GAG AAT 346
 V T D L L K K S R K L L I L V Q K K G E 69
 GTT ACA GAT CTC CTG AAG AAA AGT CGG AAG CTG TTA ATT TTG GTA CAG AAA AAG GGA GAG 406
 A T C Q H F L K C L F S T F P Q L A A I 89
 GCG ACC TGT CAG CAT TTT CTC AAG TGT TTA TTT AGT ACT TTT CCA CAG TTA GCT GCC ATT 466
 C G L R H E V L K H E N T V P P Q S M G 109
 TGC GGC TTA AGG CAT GAA GTT TTA AAA CAT GAG AAT ACA GTA CCT CCT CAA TCT ATG GGG 526
 A S S N S E D A F S P G I K Q P E A P E 129
 GCA AGC AGT AAT TCA GAA GAT GCT TTT TCT CCT GGA ATA AAA CAG CCT GAA GCC CCT GAG 586
 I T V F F S E K E H L D L E T S E F F R 149
 ATC ACA GTG TTC TTC AGT GAG AAG GAA CAC TTG GAT TTG GAA ACC TCT GAG TTT TTC AGG 646
 D K K T S Y R E T A L S A R K N E K E Y 169
 GAC AAG AAA ACT AGT TAT AGG GAA ACA GCT TTG TCT GCC AGG AAG AAT GAG AAG GAA TAT 706
 D T P E V T L S Y S V E K V G C E V P A 189
 GAC ACA CCA GAA GTC ACA TTA TCA TAT TCA GTT GAG AAA GTT GGA TGT GAA GTT CCA GCA 766
 T I T Y I K D G Q R Y E E L D D S L Y L 209
 ACT ATT ACA TAT ATA AAA GAT GGA CAG AGA TAT GAG GAG CTA GAT GAT TCT TTA TAC TTA 826
 G K E E Y L G S V D T P E D A E A T V E 229
 GGA AAA GAG GAA TAT CTA GGA TCT GTT GAC ACC CCT GAA GAT GCA GAA GCC ACT GTG GAA 886
 E E V Y D D P E H V G Y D G E E D F E N 249
 GAG GAG GTT TAT GAT GAC CCA GAG CAC GTT GGA TAT GAT GGT GAA GAG GAC TTC GAG AAT 946
 S E T T E F S G E E P S Y E G S E T S L 269
 TCA GAA ACC ACA GAG TTC TCT GGT GAA GAA CCA AGT TAT GAG GGA TCA GAA ACC AGC CTT 1006
 S L E E E Q E K S I E E R K K V F K D V 289
 TCA TTG GAG GAG GAA CAG GAG AAA AGT ATA GAA GAA AGA AAA AAG GTG TTT AAA GAT GTC 1066
 L L C L N M D R S R K V L P D F V K Q F 309
 CTG TTA TGT TTG AAC ATG GAT AGA AGC AGA AAG GTT CTG CCA GAT TTT GTT AAA CAA TTC 1126
 S L D R G C K W T P E S P G D L A W N F 329
 TCC TTA GAT CGA GGA TGT AAG TGG ACC CCT GAG AGT CCA GGA GAC TTA GCC TGG AAT TTC 1186
 L M K V Q A R D V T A R D S I L S H K V 349
 CTG ATG AAA GTT CAA GCA CGA GAT GTG ACG GCT AGG GAT TCA ATC CTC AGT CAC AAG GTT 1246
 L D E D S K E D L L A G V E N L E I R D 369
 CTG GAT GAA GAT AGC AAG GAG GAT TTG CTG GCT GGA GTG GAG AAT TTG GAA ATT CGA GAC 1306

00720734 120400

FIG. 2B (1 of 4)

[illegible]

FIG. 28 (2 OF 4)

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P F Q N A G A Q G R G K S F G I Q S F H 789
CCT TTT CAG AAT GCA GGG GCC CAG GGC CGA GGT AAA AGT TTT GGT ATT CAA TCC TTC CAT 2566

P Q I F Y S G E R F M K F S R V A R G C 809
CCC CAG ATA TTT TAT TCA GGT GAA AGA TTC ATG AAA TTT TCC AGA GTT GCT CGG GGA TGT 2626

H S N G T F G R L P R P I C Q H V Q A C 829
CAC TCG AAT GGA ACA TTT GGG AGA CTG CCA AGA CCC ATT TGT CAG CAT GTA CAG GCC TGC 2686

P E R P Q M M G T L E R S R A V A S K I 849
CCT GAG AGA CCA CAA ATG ATG GGA ACT CTT GAA AGG TCT AGG GCA GTA GCC TCC AAG ATA 2746

G H S Y S L D S Q P A R A V G K P W P Q 869
GGT CAC TCC TAT TCC CTG GAT TCA CAG CCA GCA AGA GCA GTA GGG AAG CCA TGG CCT CAG 2806

Q A C T R V T E L T E A T G K L I R T S 889
CAA GCT TGC ACC AGG GTA ACA GAG TTA ACT GAA GCA ACT GGA AAA CTG ATA AGA ACA TCC 2866

H I G K P H P Q S F Q P A A A T Q K L R 909
CAT ATT GGA AAG CCT CAC CCT CAG TCC TTT CAA CCA GCA GCA GCC ACA CAA AAA CTA AGA 2926

P A S Q Q G V Q M K T Q G G A S N P A L 929
CCT GCT TCT CAG CAA GGA GTC CAG ATG AAG ACA CAA GGT GGG GCT TCA AAT CCA GCT CTC 2986

Q I G S H P M C K S S Q F K S D Q S N P 949
CAA ATA GGG TCC CAT CCC ATG TGC AAG AGC TCT CAG TTC AAA TCC GAT CAG TCC AAC CCA 3046

S T V K H S Q P K P F H S V P S Q P K S 969
TCC ACA GTC AAA CAC TCC CAG CCT AAA CCC TTC CAT TCT GTG CCC TCT CAA CCT AAA TCC 3106

S Q T K S C Q S Q P S Q T K P S P C K S 989
TCT CAG ACA AAA TCC TGT CAG TCC CAG CCC TCC CAA ACT AAA CCT TCT CCA TGC AAA TCT 3166

T Q P K P S Q P W P P Q S K P S Q P R P 1009
ACT CAG CCT AAG CCA AGC CAG CCC TGG CCT CCC CAG TCT AAG CCT TCT CAG CCC AGA CCC 3226

P Q P K S S S T N P S Q A K A H H S K A 1029
CCT CAA CCT AAG TCA TCC TCA ACC AAT CCT TCA CAA GCT AAG GCA CAC CAC TCA AAA GCA 3286

G Q K R G G K H * 1038
GGG CAG AAG AGG GGA GGG AAG CAT TAA 3313

AGAGCTAACTCCAGAGATCTATAAAGCATATCCTTTACCCAGGCCATTCTATCATATAGTAAGCAGAAGAGTTGCCAT 3392

GAAAGTAAAAGACTACTGTTCATTAGCATGTAAAACAAAGAAAGATATACATGACCGAATTGGATATCTTTGTTTGTGTTG 3471

TTTGAGACAGAGTTTCACTCTTGTGTGCCAGGCTGGAGTGCAATGGCAGATCTCGGCTCACCGCAACCTCTGCTTCCT 3550

GGCTTAAAGTGATTCTCCTGCCTCAGCCTCTCGAGTAGCTGGGATTACAGGCATGCACCACCACACCCAGCTAATTTTG 3629

TATTTTATAGTAGAGGCAGGGTTTCTCCATGTTGGTCAGGCTGGTCTTGAACCTCCCGACCTCAGGTGATCCGCCCCACCTA 3708

GGCCTCTCAAAGTGTGGGATTACGTGTGTAAGCCACAGTGGCCAGCCGAATTGGATATCTTTAAGATATCTGTAAGT 3787

GTTATATCCCTAACCAAGAAGAAAAATATGAAAATAATTAAGACTAGAAATCAAGCAGTAGATAATTGAATCCAATCTTG 3866

GGTATTATTAGATAATGTATAACTTGCACCCAGGGAATGGGGGTCTATGAGACAACCCCACTTGGAGAAGAATGGGGTT 3945

AGGGTCTCTAATTGCAAAGTGACTGTACAATAGGACGAAAGTTGCCTCTGTGTCTGAGAAAGTATCTTAGTTGTTGGCT 4024

GCTCCAGAGGTATCTTTGTCAAAAGCTTCTGGTTCAATATCAGCCACTGAGCAGATAACCCCTGCTTATTGGTGTTGGTT 4103

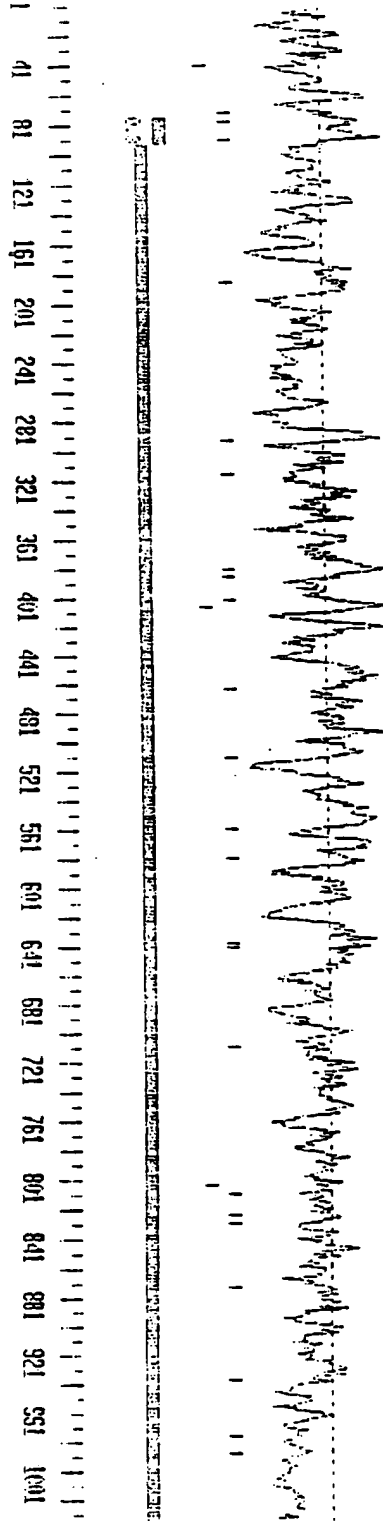
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ATGAATTAAACAACCAATAAAATTAATCATTTGGCATTAAAAAAAAAAAAAAAAAAAAA 4244

[illegible]

56/58

Ch
Mly
24
14
13



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FIG. 29

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09720721 120400

CONSENSUS *->maederrlLkknrvrliesLgldvLdelLdvLlekdvlnlkeeEkik
 +++ + ** r++l+e+L+ d d +Ld L +++++ ++e E
CARD6 5 STP--SEIIERERKKLLEILQHD-PDSILDTLTSRRLISEEEYETLE 48

CONSENSUS ragakledDKarelvdslqrrgsqafdafidaledTgqsyLAdvLel<-*
 + l + r l++ +q++g. + ++ f+ +l++ LA++ +l
CARD6 49 NVTDLLKK--SRKLLILVQKKGEATCQHFLKCLFS-TFPQLAAICGL 92

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- A - E S - G S E I I D Q H R X A L L A R V T E D P - D S L L D A L L S R D L I Majority

10 20 30 40

1 I A Q Q W - - - - I Q S K P E D I V N Q M T E A C L N Q S L D A L L S R D L I hCARD3-CARD

1 - - - E S H P H I Q L L K S N R E L L V T H I R N T - Q C I V I N L L K N Y Y hCARD4-CARD

1 - - - - C L H F I D O H E A A L I A R V T N - - V E W I L D A I V G K - V L hCARD5-CARD

1 - - - - C - H F V D O H E A A L I A R V T E - - V I G V L D A I H G S - V L hCARD5-CARD

1 M A T E S T P S E I I E R E R K K L L E I L Q H D P - D S I L E T L T S E R L I hCARD6-CARD

1 M A S E G A S S E I I E K Q E T K L L S V L Q Q D P - D S I L E T L T S E R L I hCARD6-CARD

S E E D Y E A V E A E T T X L S K V R K L L I L V O S K G E E T C K - F L K C L Majority

50 60 70 80

36 M K E D Y E L V S T K P T R T S K V R Q L L D T T D I O G E E - - - - I A V I hCARD3-CARD

37 S A E D A F I V C A C P T Q P D K V R E I I D L V O S K G E E V S E F E I - Y I hCARD4-CARD

32 T D E Q Y Q A V R A E P T N P S K M R K L F S F T P A W - N W T C E - - - D L I hCARD5-CARD

31 T E G Q Y Q A V R A E T T S O D I M R K L F S F V P S W - N L T C E - - - D S I hCARD5-CARD

40 S E E E Y E T L I N V T D L L K E S R K L L I L V Q K K G E A T C Q H F L K C L hCARD6-CARD

40 S E E E Y E T L E A I I D P L K E S R K L L I L I C K E G E D S C C E L E C L hCARD6-CARD

L Q A L K D S A A Y L G L D P E V - - - - - L E - S Majority

90 100

72 V Q K L K D N K O - M G I Q P Y P - - - - - I I L hCARD3-CARD

76 L Q Q L A F - - A V V D I R P W L hCARD4-CARD

68 L Q A L R E S Q S Y L V E E - - - - - L E R S hCARD5-CARD

67 L Q A L E I H P T L V M E - - - - - L E Q S hCARD5-CARD

80 F S T F P Q L A E I C G L R H E V L hCARD6-CARD

80 S N A F P Q S A S T L G I K Q E V P R Q G T G E V V E V S hCARD6-CARD

FIG. 31